wwPDB X-ray Structure Validation Summary Report (i)

Aug 5, 2026 – 04:37 PM EDT

PDB ID	:	4V9S / pdb_00004v9s
Title	:	Crystal structure of antibiotic GE82832 bound to 70S ribosome
Authors	:	Bulkley, D.P.; Brandi, L.; Polikanov, Y.S.; Fabbretti, A.; O'Connor, M.; Gualerzi, C.O.; Steitz, T.A.
Deposited on	:	2013-12-05
Resolution	:	3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

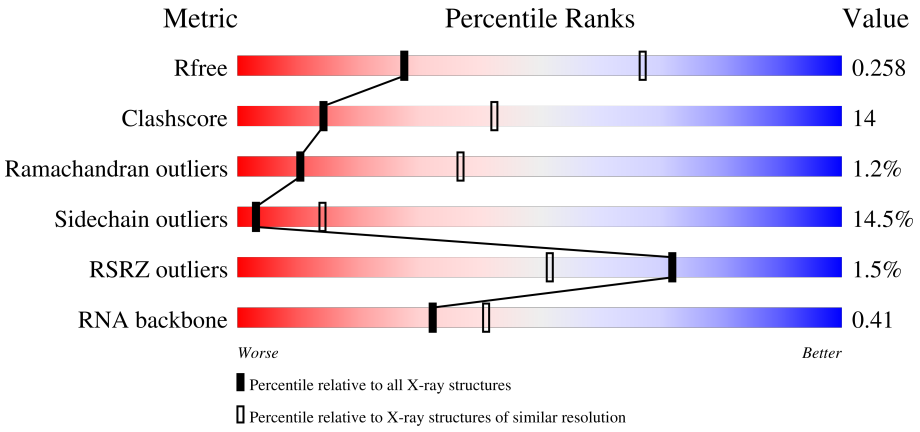
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

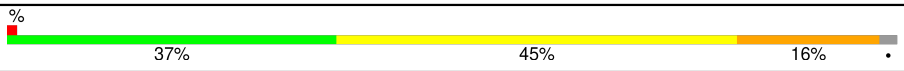
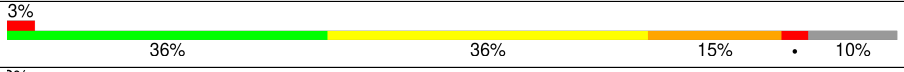
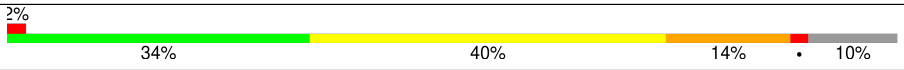
The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1522	
1	CA	1522	
2	AB	256	
2	CB	256	

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Mol	Chain	Length	Quality of chain
3	AC	239	2% 49% 33% 5% 14%
3	CC	239	3% 48% 31% 8% 14%
4	AD	209	3% 49% 37% 11%
4	CD	209	% 52% 36% 11%
5	AE	162	% 46% 38% 7% 9%
5	CE	162	% 51% 37% 9%
6	AF	101	55% 37% 7%
6	CF	101	% 60% 34% 5%
7	AG	156	% 58% 32% 8%
7	CG	156	4% 53% 36% 11%
8	AH	138	% 53% 36% 10%
8	CH	138	53% 38% 8%
9	AI	128	7% 49% 40% 9%
9	CI	128	22% 42% 48% 9%
10	AJ	105	6% 50% 35% 7% 8%
10	CJ	105	15% 45% 41% 5% 9%
11	AK	129	% 64% 20% 5% 12%
11	CK	129	53% 35% 12%
12	AL	132	4% 60% 27% 5% 8%
12	CL	132	% 56% 30% 6% 8%
13	AM	126	2% 64% 27% 6%
13	CM	126	6% 48% 40% 8%
14	AN	61	10% 52% 36% 10%
14	CN	61	15% 49% 44% 5%
15	AO	89	% 66% 28%

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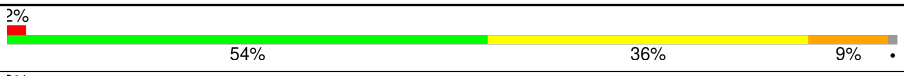
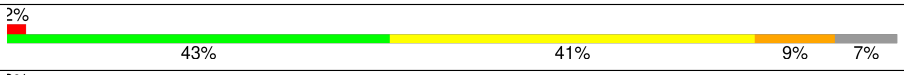
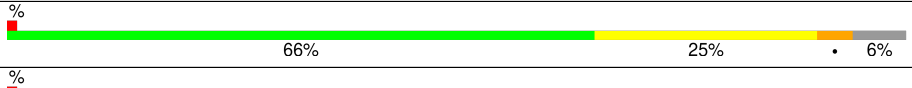
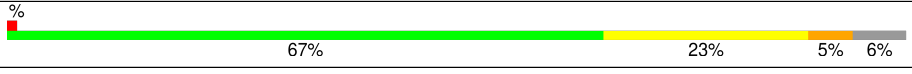
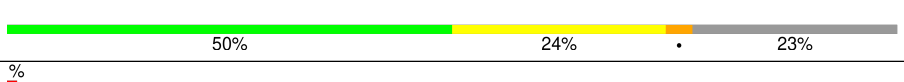
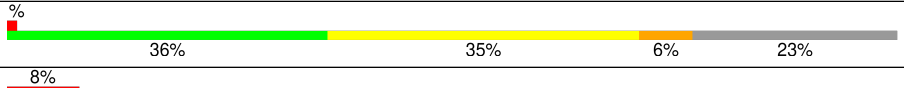
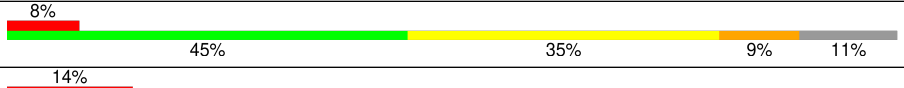
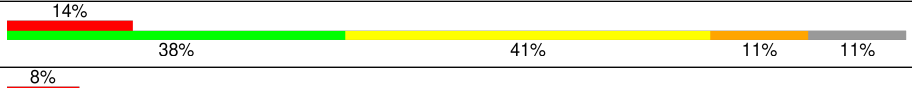
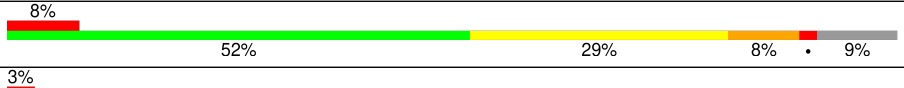
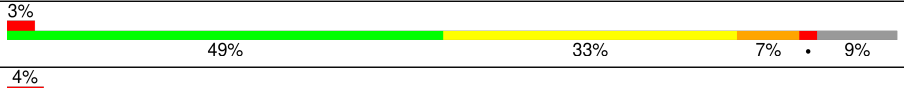
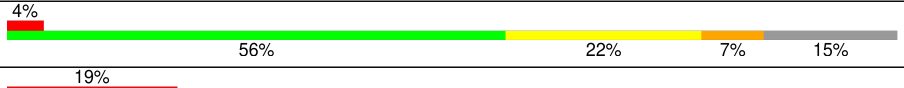
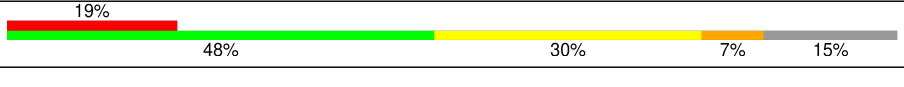
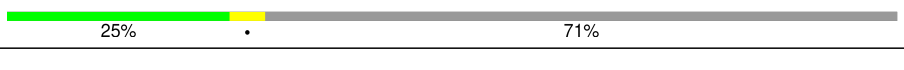
Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AX	77	
23	CX	77	
24	AW	10	
24	CW	10	
25	BA	2915	
25	DA	2915	
26	BB	122	
26	DB	122	
27	BD	276	
27	DD	276	

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Mol	Chain	Length	Quality of chain
28	BE	206	67% 23% 8%
28	DE	206	59% 31% 8%
29	BF	210	61% 30% 5%
29	DF	210	56% 33% 8%
30	BG	182	58% 35% 7%
30	DG	182	42% 45% 12%
31	BH	180	61% 27% 8%
31	DH	180	51% 38% 8%
32	BI	148	47% 39% 11%
32	DI	148	55% 35% 8%
33	BN	140	74% 21%
33	DN	140	66% 29%
34	BO	122	68% 28%
34	DO	122	57% 39%
35	BP	150	67% 27% 5%
35	DP	150	59% 32% 9%
36	BQ	141	60% 33% 7%
36	DQ	141	53% 40% 6%
37	BR	118	64% 26% 9%
37	DR	118	57% 37% 6%
38	BS	112	65% 25% 7%
38	DS	112	43% 45% 11%
39	BT	146	59% 28% 10%
39	DT	146	58% 27% 10%
40	BU	118	68% 27%

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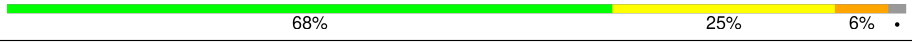
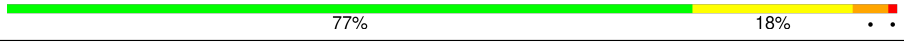
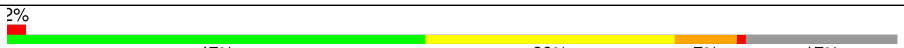
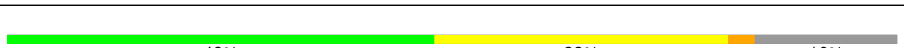
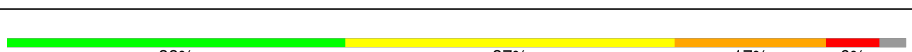
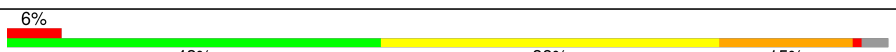
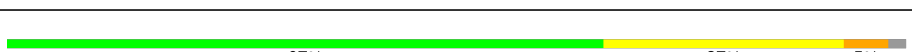
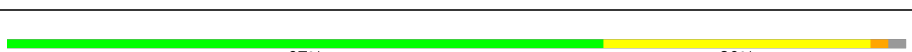
Mol	Chain	Length	Quality of chain
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	
51	B5	60	
51	D5	60	
52	B6	54	
52	D6	54	

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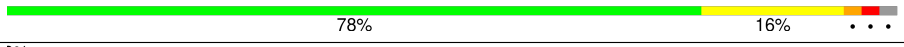
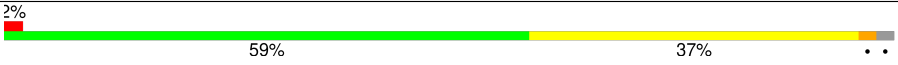
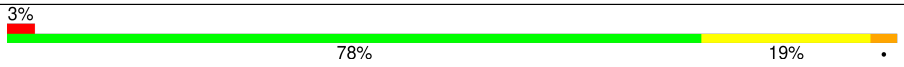
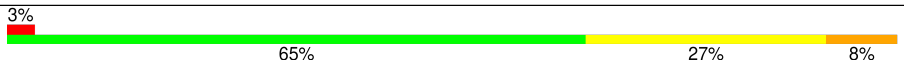
Mol	Chain	Length	Quality of chain
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	2QY	CW	10	-	-	X	-
24	MVA	CW	9	-	-	X	-
56	MG	AA	3030	-	-	-	X
56	MG	AA	3084	-	-	-	X
56	MG	BA	3180	-	-	-	X
56	MG	CA	3053	-	-	-	X

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 286321 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1498	Total	C	N	O	P	0	0	0
			32196	14328	5966	10404	1498			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
2	CB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
5	CE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
8	CH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			983	623	193	167			
9	CI	127	Total	C	N	O	0	0	0
			978	619	190	169			

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	AJ	97	Total	C	N	O	0	0	0
			709	440	138	131			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total 714	C 445	N 138	O 131	0	0	0

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	114	Total 829	C 516	N 155	O 155	S 3	0	0	0
11	CK	114	Total 833	C 519	N 156	O 155	S 3	0	0	0

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	122	Total 930	C 585	N 185	O 159	S 1	0	0	0
12	CL	122	Total 930	C 585	N 185	O 159	S 1	0	0	0

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	123	Total 958	C 592	N 198	O 166	S 2	0	0	0
13	CM	122	Total 950	C 586	N 197	O 165	S 2	0	0	0

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	60	Total 492	C 312	N 104	O 72	S 4	0	0	0
14	CN	60	Total 492	C 312	N 104	O 72	S 4	0	0	0

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AO	88	Total 728	C 456	N 144	O 126	S 2	0	0	0
15	CO	88	Total 728	C 456	N 144	O 126	S 2	0	0	0

- Molecule 16 is a protein called 30S Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
16	CP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	68	Total	C	N	O	0	0	0
			555	355	108	92			
18	CR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	CU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	7	Total	C	N	O	P	0	0	1
			114	49	22	37	6			
22	CV	6	Total	C	N	O	P	0	0	0
			113	49	22	36	6			

- Molecule 23 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AX	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			
23	CX	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			

- Molecule 24 is a protein called GE82832.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	AW	10	Total	C	N	O	0	0	0
			93	67	10	16			
24	CW	10	Total	C	N	O	0	0	0
			93	67	10	16			

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2731	Total	C	N	O	P	0	0	0
			58834	26185	11020	18899	2730			
25	DA	2714	Total	C	N	O	P	0	0	0
			58458	26018	10942	18786	2712			

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 27 is a protein called 50S Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
27	DD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 28 is a protein called 50S Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
28	DE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 29 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
29	DF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 30 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BG	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
30	DG	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 31 is a protein called 50S Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
31	DH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 32 is a protein called 50S Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BI	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
32	DI	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 33 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
33	DN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 34 is a protein called 50S Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
34	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 35 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
35	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 36 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
36	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 37 is a protein called 50S Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
37	DR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 38 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
38	BS	110	Total	C	N	O	0	0	0
			877	553	175	149			
38	DS	110	Total	C	N	O	0	0	0
			870	549	173	148			

- Molecule 39 is a protein called 50S Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
39	DT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 40 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
40	DU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 41 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
41	DV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 42 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	DW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 43 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
43	DX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 44 is a protein called 50S Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
44	DY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 45 is a protein called 50S Ribosomal Protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BZ	171	Total	C	N	O	S	0	0	0
			1349	862	243	242	2			
45	DZ	174	Total	C	N	O	S	0	0	0
			1360	870	243	245	2			

- Molecule 46 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
46	D0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 47 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
47	D1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 48 is a protein called 50S Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
48	D2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 49 is a protein called 50S Ribosomal Protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B3	59	Total	C	N	O	0	0	0
			469	298	90	81			
49	D3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 50 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			551	348	99	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			531	338	97	91	5			

- Molecule 51 is a protein called 50S Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
51	D5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 52 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
52	D6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 53 is a protein called 50S Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
53	D7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 54 is a protein called 50S Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B8	64	Total	C	N	O	S	0	0	0
			511	328	99	82	2			
54	D8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 55 is a protein called 50S Ribosomal Protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	D9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AA	221	Total	Mg	0	0
			221	221		
56	AD	1	Total	Mg	0	0
			1	1		
56	AF	1	Total	Mg	0	0
			1	1		
56	AK	1	Total	Mg	0	0
			1	1		
56	AM	1	Total	Mg	0	0
			1	1		
56	AN	2	Total	Mg	0	0
			2	2		
56	AV	1	Total	Mg	0	0
			1	1		
56	AX	9	Total	Mg	0	0
			9	9		
56	BA	738	Total	Mg	0	0
			738	738		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	BB	18	Total Mg 18 18	0	0
56	BD	12	Total Mg 12 12	0	0
56	BE	10	Total Mg 10 10	0	0
56	BF	8	Total Mg 8 8	0	0
56	BG	4	Total Mg 4 4	0	0
56	BN	6	Total Mg 6 6	0	0
56	BO	1	Total Mg 1 1	0	0
56	BP	4	Total Mg 4 4	0	0
56	BQ	5	Total Mg 5 5	0	0
56	BR	4	Total Mg 4 4	0	0
56	BU	8	Total Mg 8 8	0	0
56	BV	4	Total Mg 4 4	0	0
56	BW	5	Total Mg 5 5	0	0
56	BX	1	Total Mg 1 1	0	0
56	BY	1	Total Mg 1 1	0	0
56	BZ	1	Total Mg 1 1	0	0
56	B0	4	Total Mg 4 4	0	0
56	B1	1	Total Mg 1 1	0	0
56	B2	1	Total Mg 1 1	0	0
56	B3	3	Total Mg 3 3	0	0
56	B4	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	B5	1	Total Mg 1 1	0	0
56	B7	4	Total Mg 4 4	0	0
56	B8	3	Total Mg 3 3	0	0
56	B9	1	Total Mg 1 1	0	0
56	CA	172	Total Mg 172 172	0	0
56	CE	2	Total Mg 2 2	0	0
56	CF	1	Total Mg 1 1	0	0
56	CQ	1	Total Mg 1 1	0	0
56	CT	1	Total Mg 1 1	0	0
56	CX	3	Total Mg 3 3	0	0
56	DA	653	Total Mg 653 653	0	0
56	DB	12	Total Mg 12 12	0	0
56	DD	8	Total Mg 8 8	0	0
56	DE	6	Total Mg 6 6	0	0
56	DF	6	Total Mg 6 6	0	0
56	DG	1	Total Mg 1 1	0	0
56	DN	1	Total Mg 1 1	0	0
56	DO	1	Total Mg 1 1	0	0
56	DQ	5	Total Mg 5 5	0	0
56	DR	2	Total Mg 2 2	0	0
56	DV	4	Total Mg 4 4	0	0

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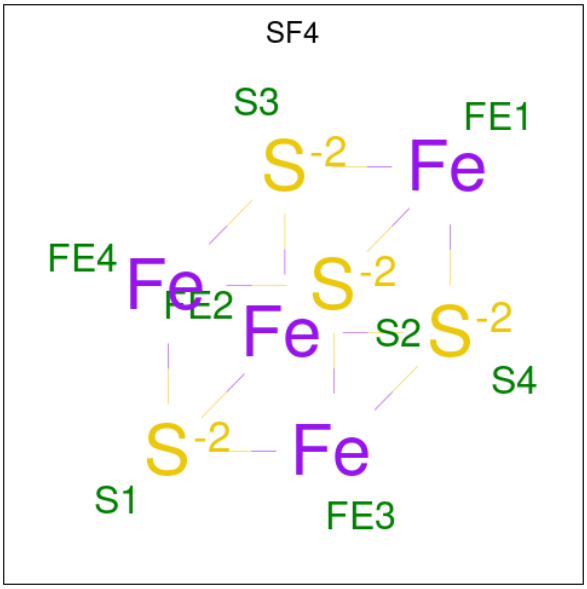
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	DW	2	Total Mg 2 2	0	0
56	DY	1	Total Mg 1 1	0	0
56	D0	1	Total Mg 1 1	0	0
56	D3	1	Total Mg 1 1	0	0
56	D5	2	Total Mg 2 2	0	0
56	D8	1	Total Mg 1 1	0	0

- Molecule 57 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AD	1	Total Fe S 8 4 4	0	0
57	CD	1	Total Fe S 8 4 4	0	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	AN	1	Total Zn 1 1	0	0

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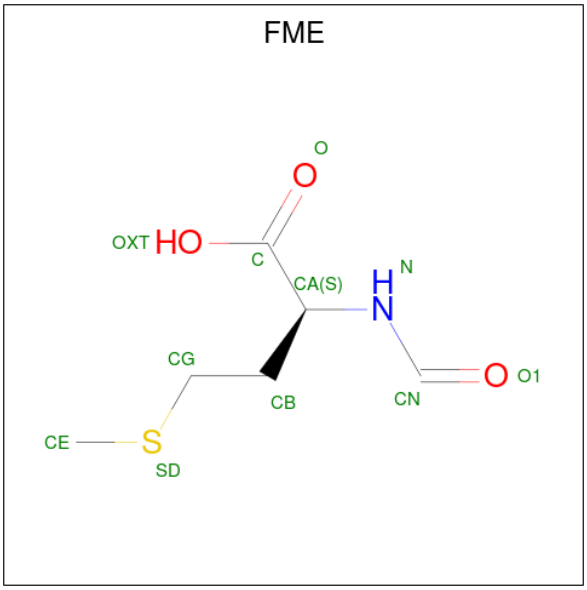
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	BY	1	Total Zn 1 1	0	0
58	B4	1	Total Zn 1 1	0	0
58	B5	1	Total Zn 1 1	0	0
58	B6	1	Total Zn 1 1	0	0
58	B9	1	Total Zn 1 1	0	0
58	CN	1	Total Zn 1 1	0	0
58	DY	1	Total Zn 1 1	0	0
58	D4	1	Total Zn 1 1	0	0
58	D5	1	Total Zn 1 1	0	0
58	D6	1	Total Zn 1 1	0	0
58	D9	1	Total Zn 1 1	0	0

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	AX	1	Total C N O S 10 6 1 2 1	0	0
59	CX	1	Total C N O S 10 6 1 2 1	0	0

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	BA	1	Total K 1 1	0	0
60	DA	1	Total K 1 1	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AA	148	Total O 148 148	0	0
61	AD	1	Total O 1 1	0	0
61	AE	3	Total O 3 3	0	0
61	AJ	1	Total O 1 1	0	0
61	AL	1	Total O 1 1	0	0
61	AP	1	Total O 1 1	0	0
61	AU	1	Total O 1 1	0	0
61	AV	1	Total O 1 1	0	0
61	AX	1	Total O 1 1	0	0
61	BA	1092	Total O 1092 1092	0	0
61	BB	26	Total O 26 26	0	0
61	BD	8	Total O 8 8	0	0
61	BE	9	Total O 9 9	0	0
61	BF	4	Total O 4 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	BG	1	Total O 1 1	0	0
61	BN	3	Total O 3 3	0	0
61	BO	2	Total O 2 2	0	0
61	BP	15	Total O 15 15	0	0
61	BQ	3	Total O 3 3	0	0
61	BR	1	Total O 1 1	0	0
61	BT	1	Total O 1 1	0	0
61	BU	4	Total O 4 4	0	0
61	BV	2	Total O 2 2	0	0
61	BW	2	Total O 2 2	0	0
61	BX	4	Total O 4 4	0	0
61	B0	4	Total O 4 4	0	0
61	B1	2	Total O 2 2	0	0
61	B5	3	Total O 3 3	0	0
61	B7	1	Total O 1 1	0	0
61	B8	8	Total O 8 8	0	0
61	CA	187	Total O 187 187	0	0
61	CE	2	Total O 2 2	0	0
61	CN	1	Total O 1 1	0	0
61	CT	1	Total O 1 1	0	0
61	CX	2	Total O 2 2	0	0

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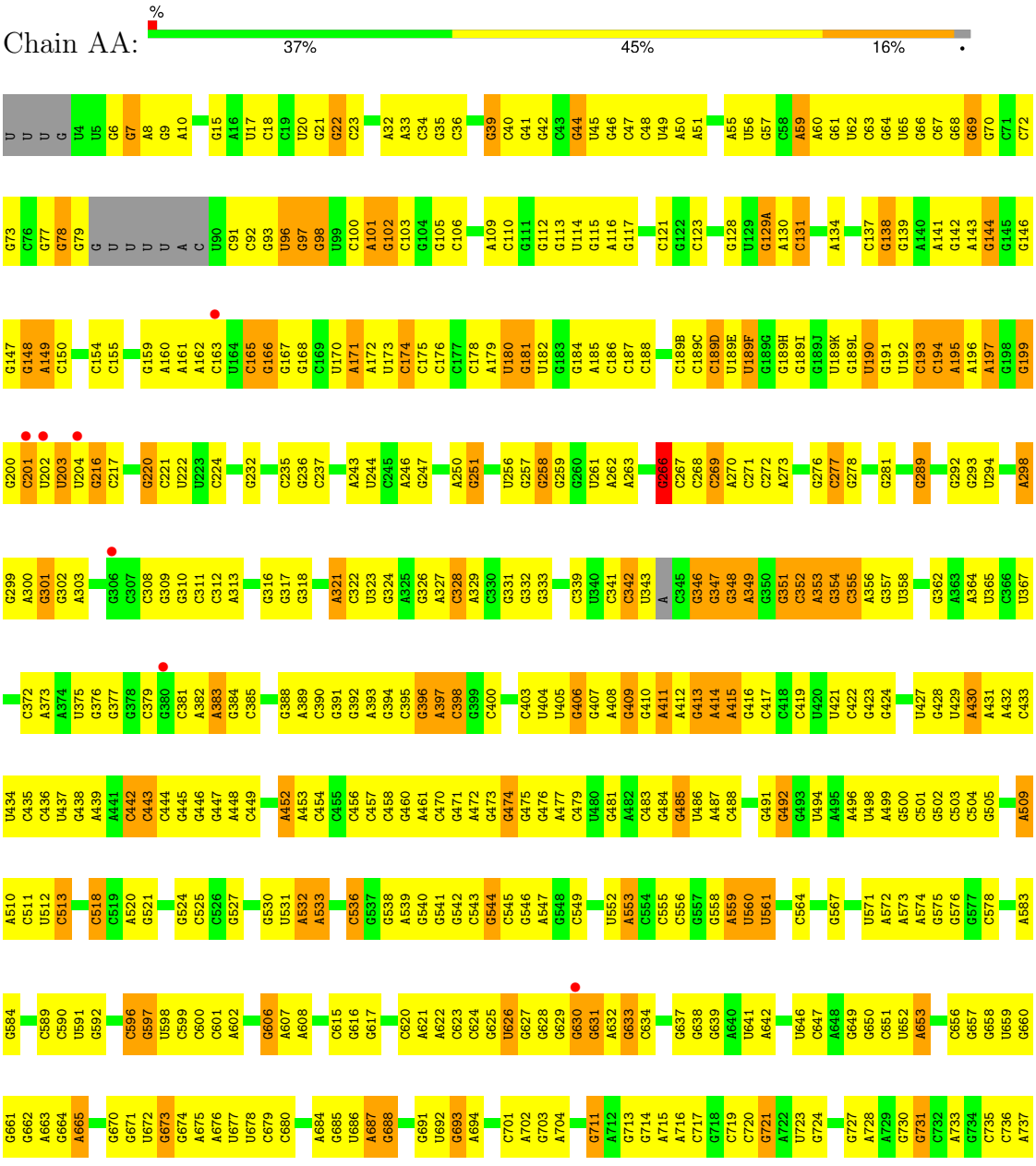
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	DA	902	Total O 902 902	0	0
61	DB	7	Total O 7 7	0	0
61	DD	8	Total O 8 8	0	0
61	DE	13	Total O 13 13	0	0
61	DF	5	Total O 5 5	0	0
61	DO	1	Total O 1 1	0	0
61	DP	14	Total O 14 14	0	0
61	DQ	3	Total O 3 3	0	0
61	DU	4	Total O 4 4	0	0
61	DV	1	Total O 1 1	0	0
61	DX	2	Total O 2 2	0	0
61	DY	2	Total O 2 2	0	0
61	D0	5	Total O 5 5	0	0
61	D1	1	Total O 1 1	0	0
61	D7	2	Total O 2 2	0	0
61	D8	4	Total O 4 4	0	0

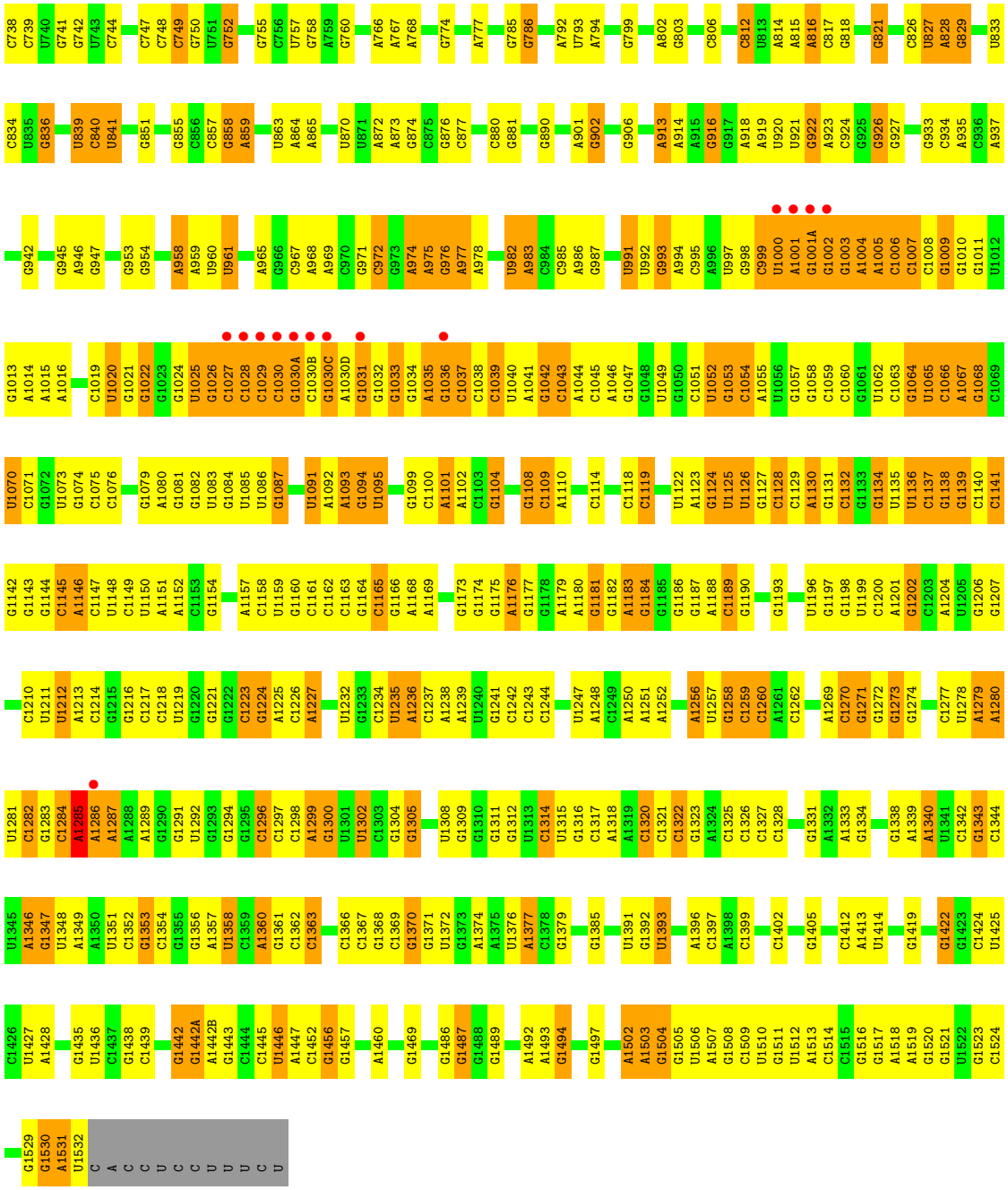
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S Ribosomal RNA

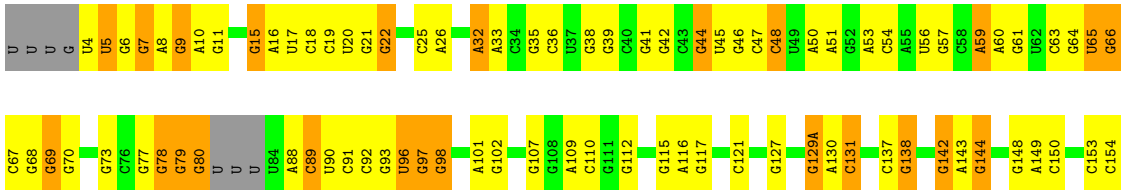
Chain AA:

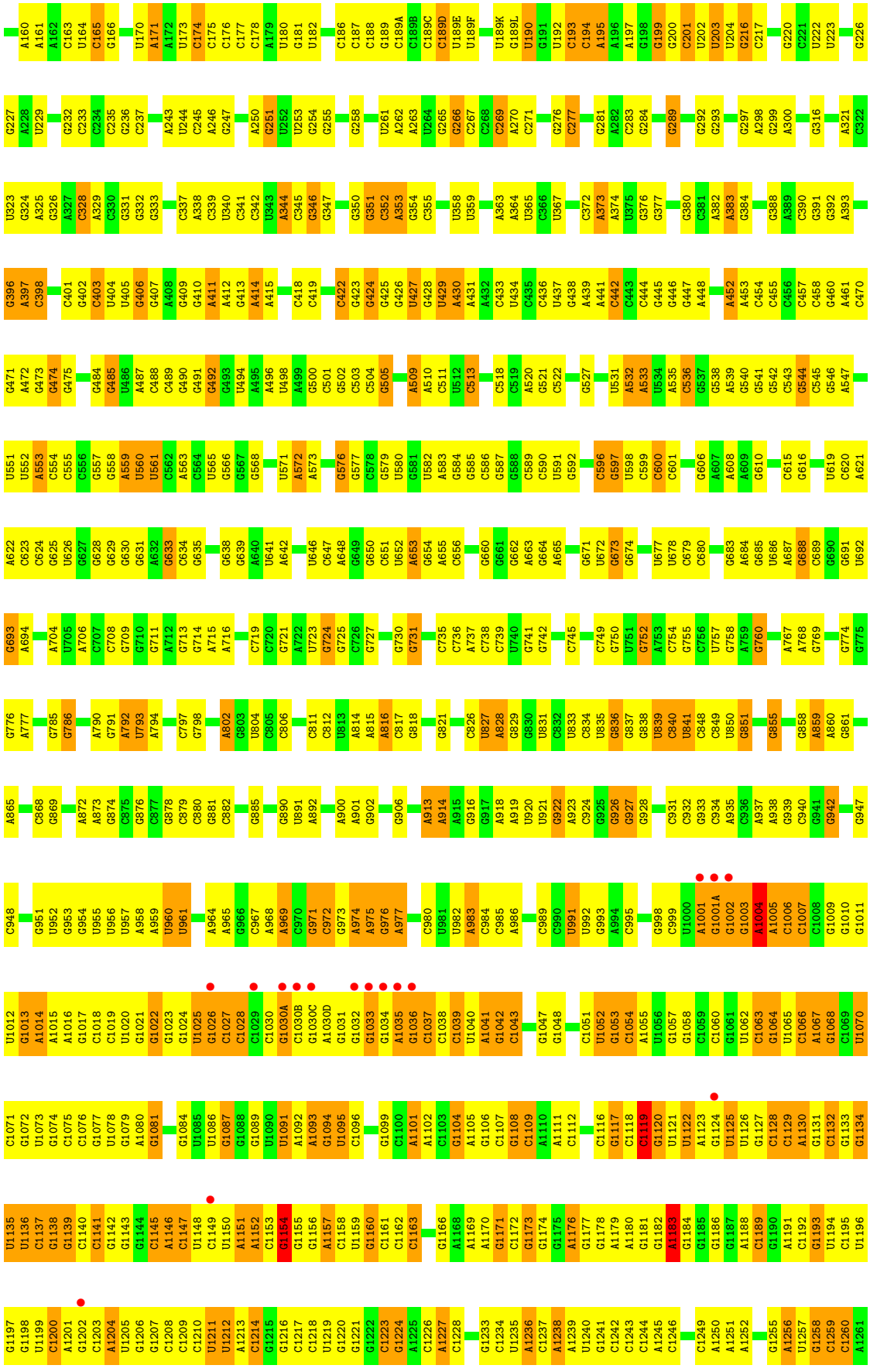


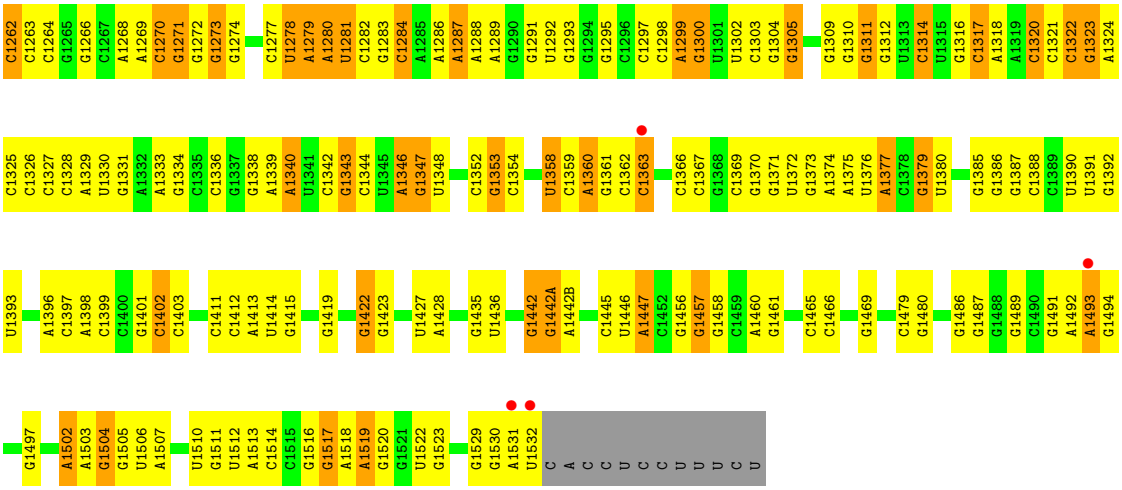


• Molecule 1: 16S Ribosomal RNA

Chain CA:

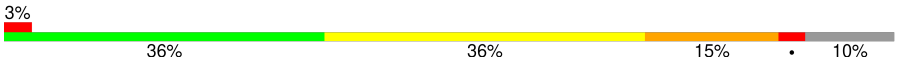


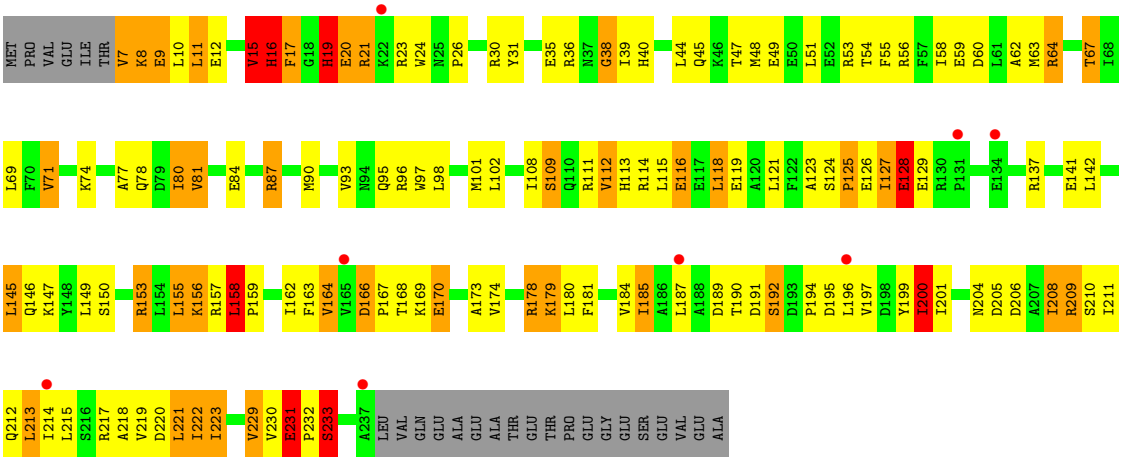




• Molecule 2: 30S Ribosomal Protein S2

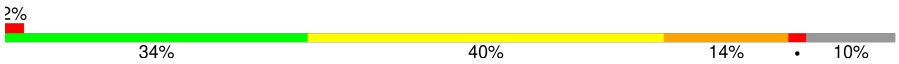
Chain AB:

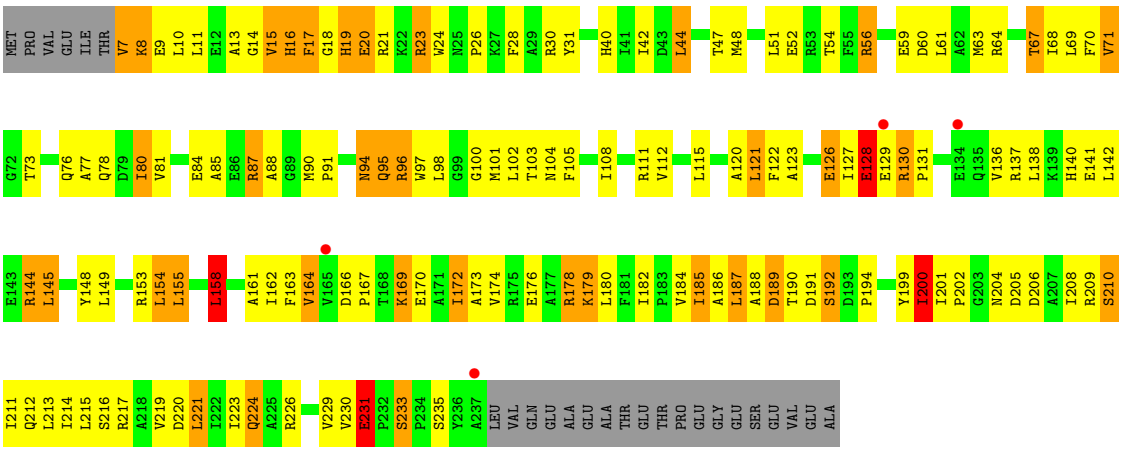




• Molecule 2: 30S Ribosomal Protein S2

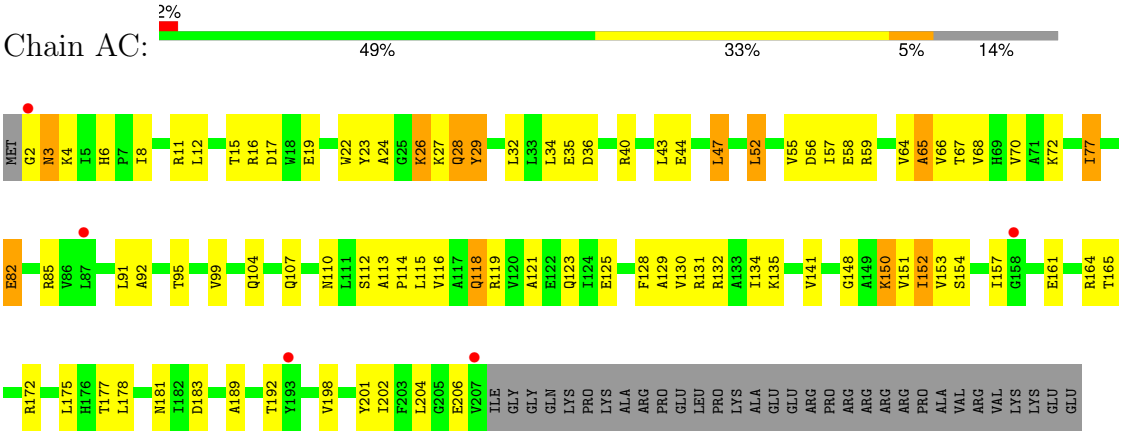
Chain CB:





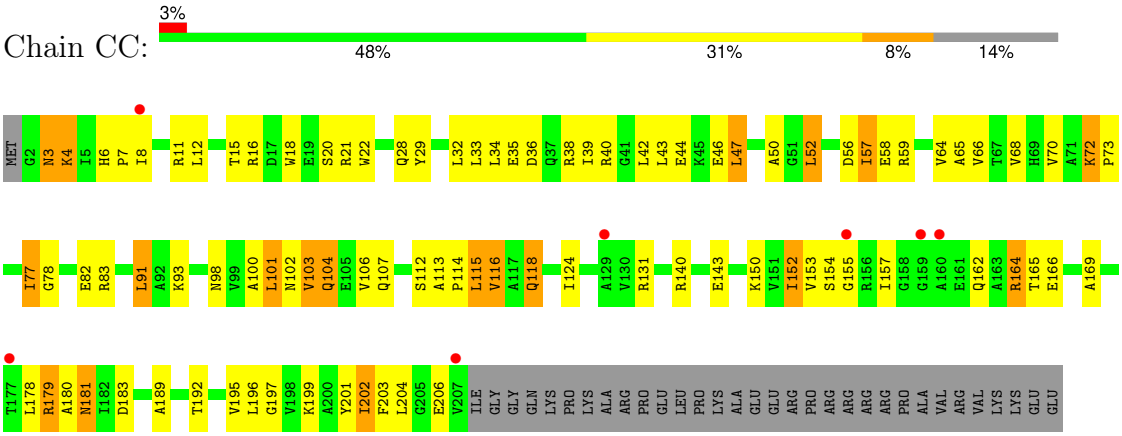
• Molecule 3: 30S Ribosomal Protein S3

Chain AC:



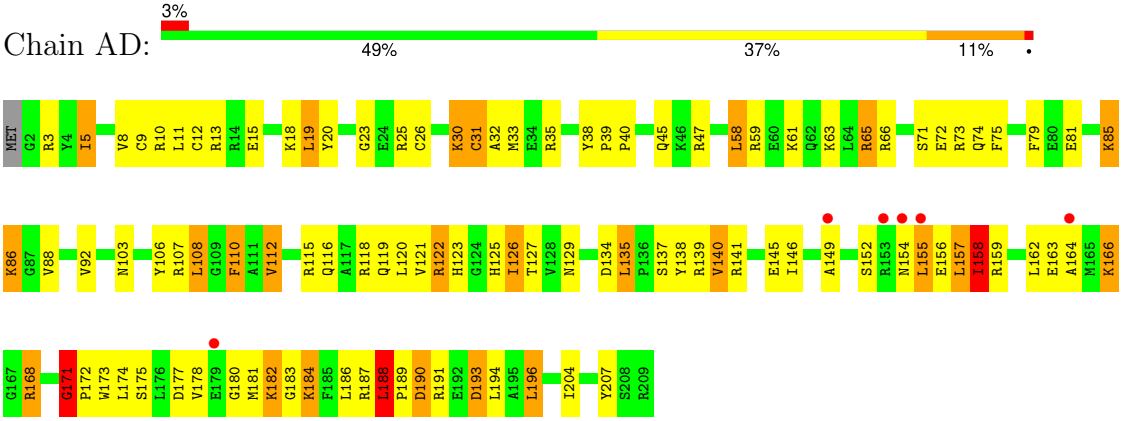
• Molecule 3: 30S Ribosomal Protein S3

Chain CC:



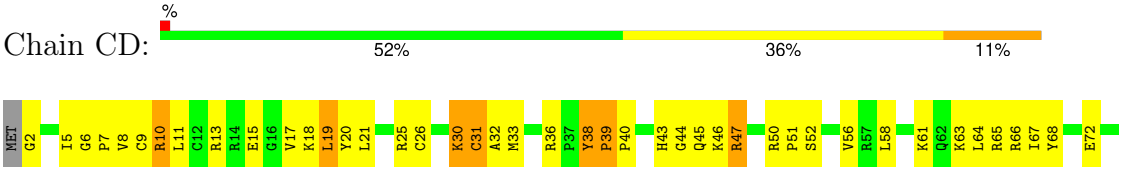
• Molecule 4: 30S Ribosomal Protein S4

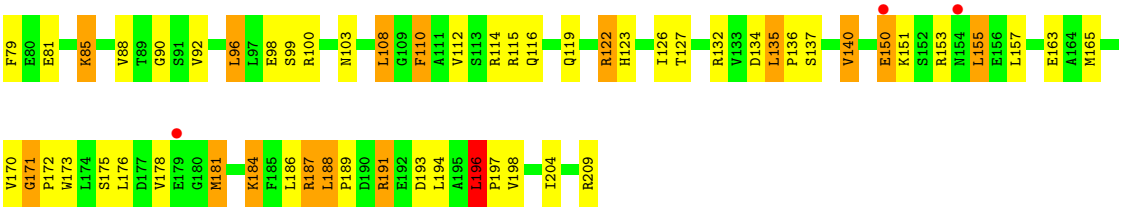
Chain AD:



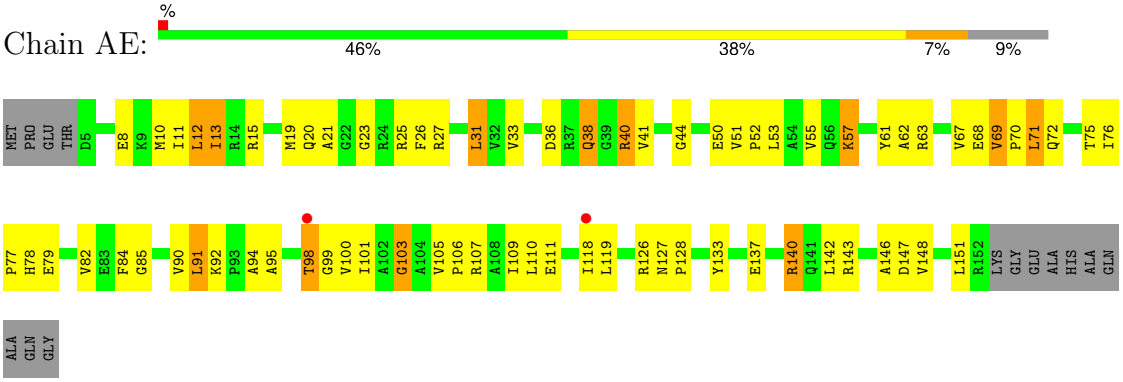
• Molecule 4: 30S Ribosomal Protein S4

Chain CD:

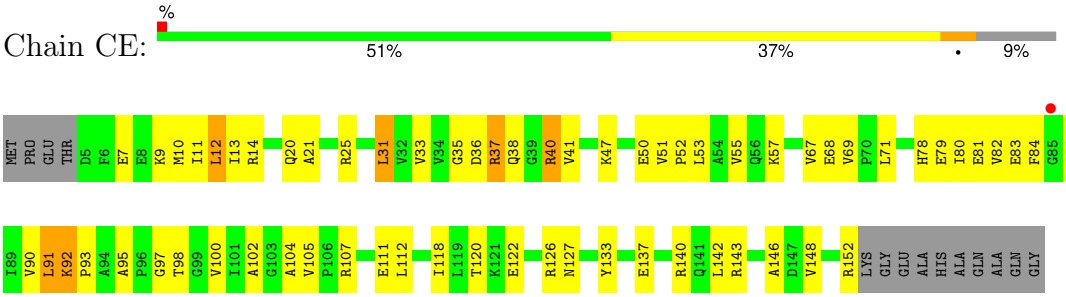




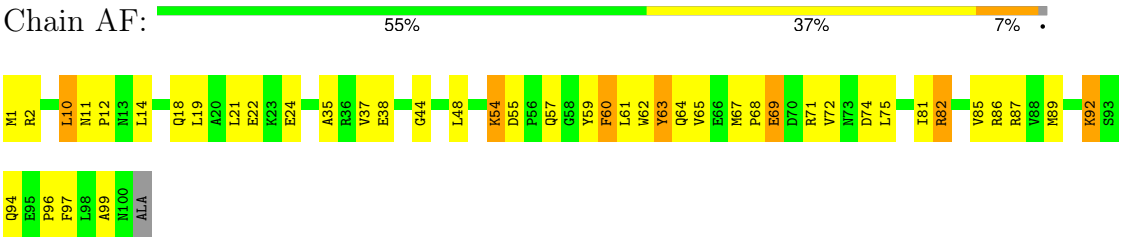
• Molecule 5: 30S Ribosomal Protein S5



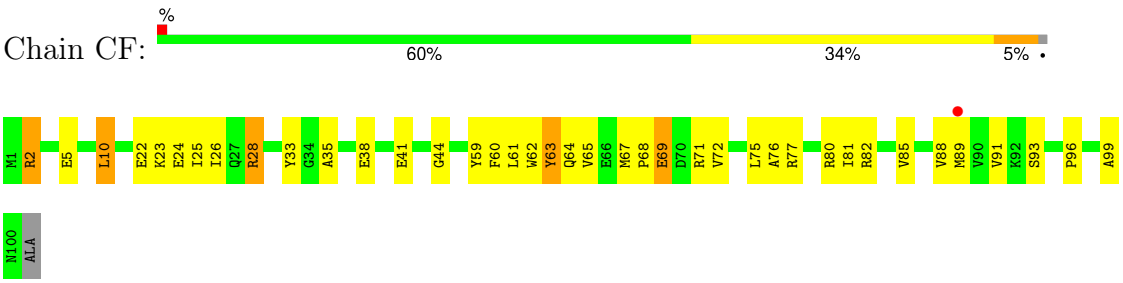
• Molecule 5: 30S Ribosomal Protein S5



• Molecule 6: 30S Ribosomal Protein S6

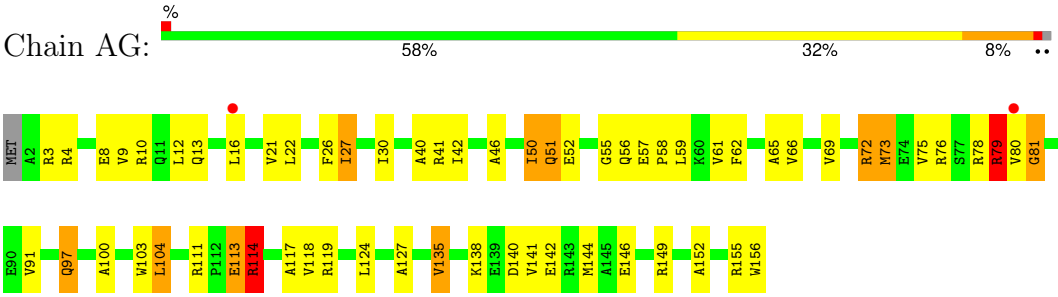


• Molecule 6: 30S Ribosomal Protein S6



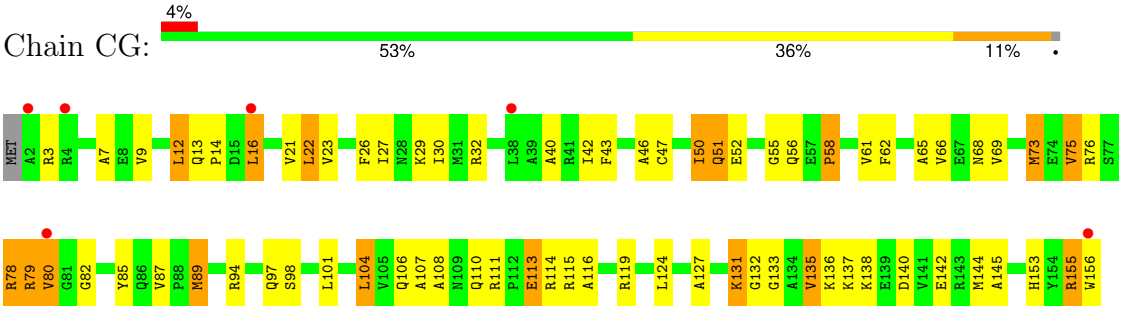
• Molecule 7: 30S Ribosomal Protein S7

Chain AG:



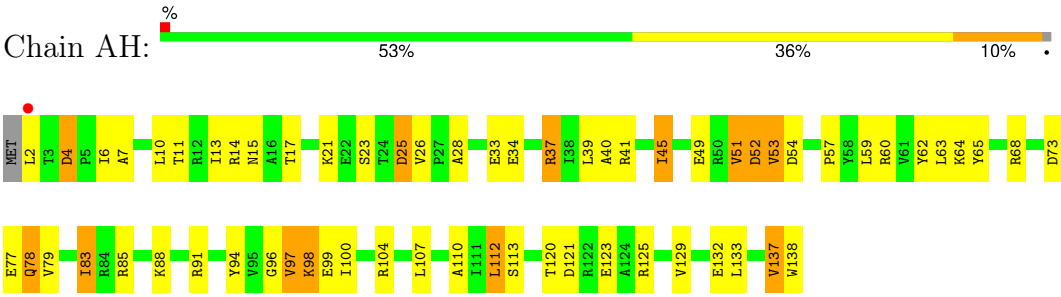
• Molecule 7: 30S Ribosomal Protein S7

Chain CG:



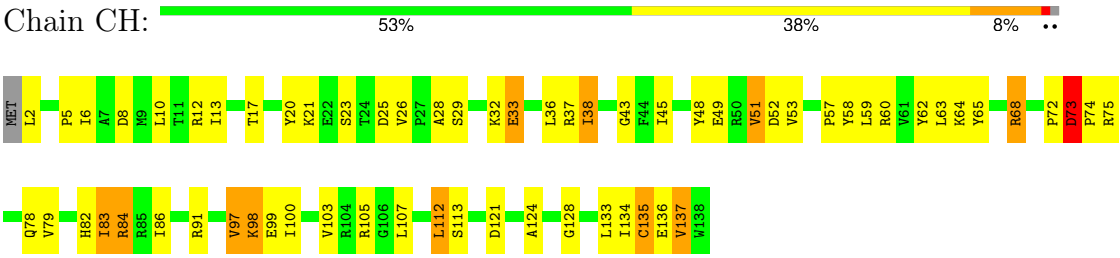
• Molecule 8: 30S Ribosomal Protein S8

Chain AH:



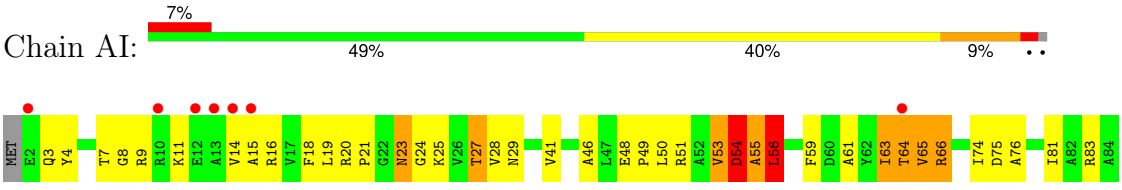
• Molecule 8: 30S Ribosomal Protein S8

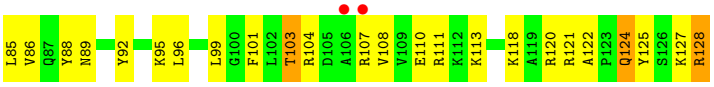
Chain CH:



• Molecule 9: 30S Ribosomal Protein S9

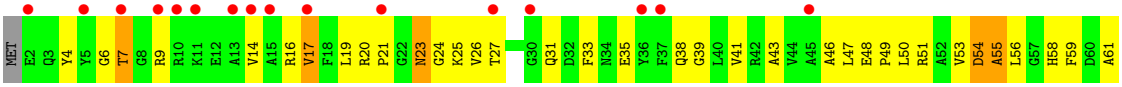
Chain AI:

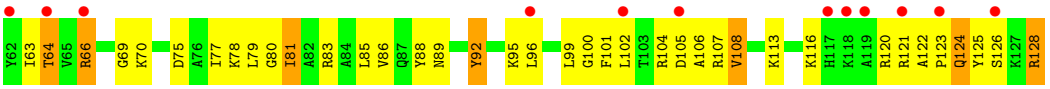




• Molecule 9: 30S Ribosomal Protein S9

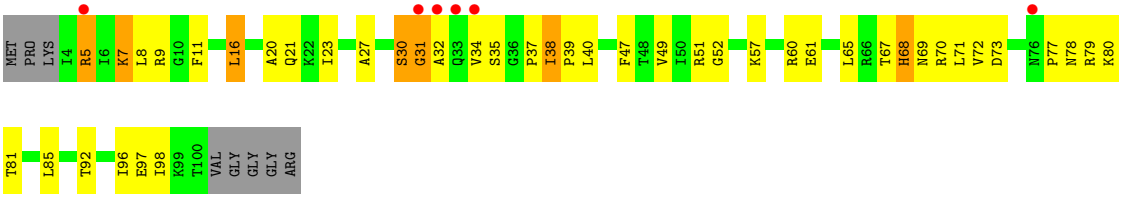
Chain CI:





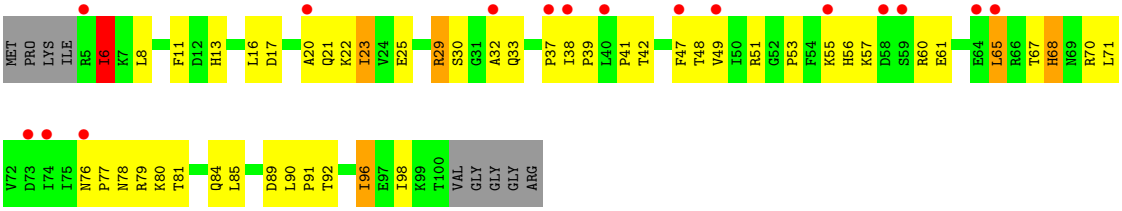
• Molecule 10: 30S Ribosomal Protein S10

Chain AJ:



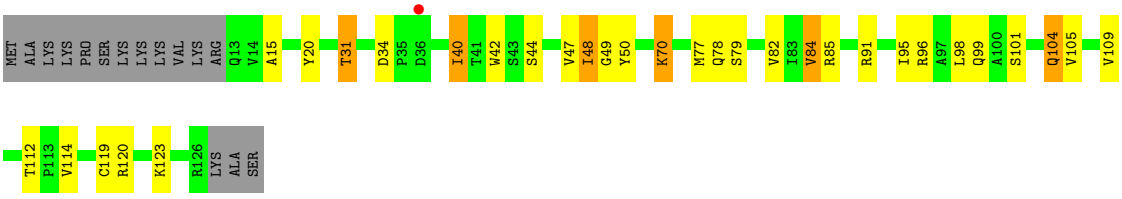
• Molecule 10: 30S Ribosomal Protein S10

Chain CJ:



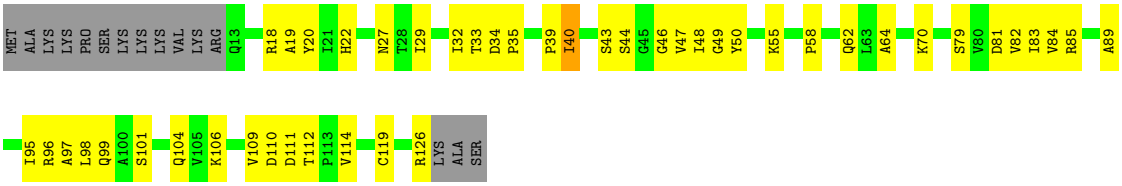
• Molecule 11: 30S Ribosomal Protein S11

Chain AK:



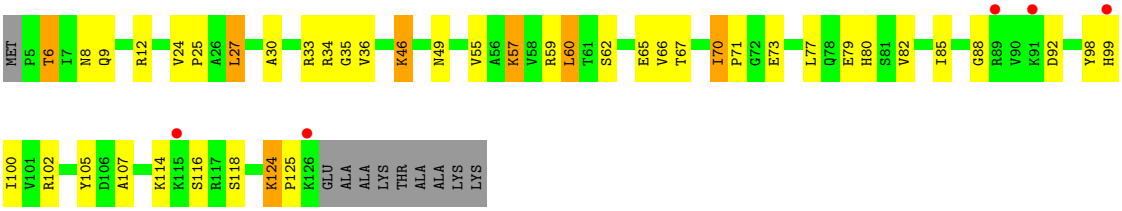
• Molecule 11: 30S Ribosomal Protein S11

Chain CK:



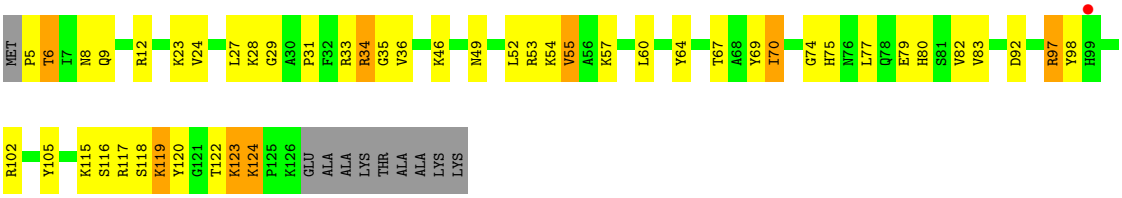
• Molecule 12: 30S Ribosomal Protein S12

Chain AL:



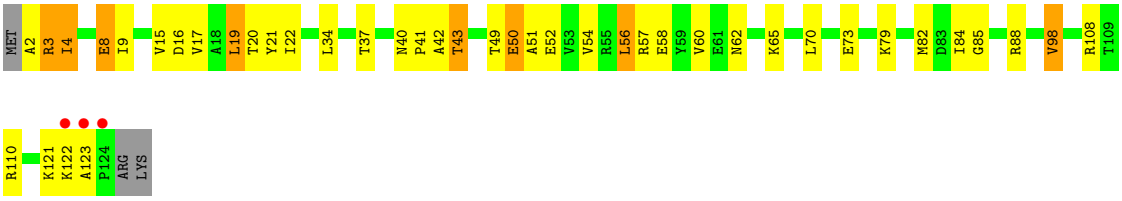
• Molecule 12: 30S Ribosomal Protein S12

Chain CL:



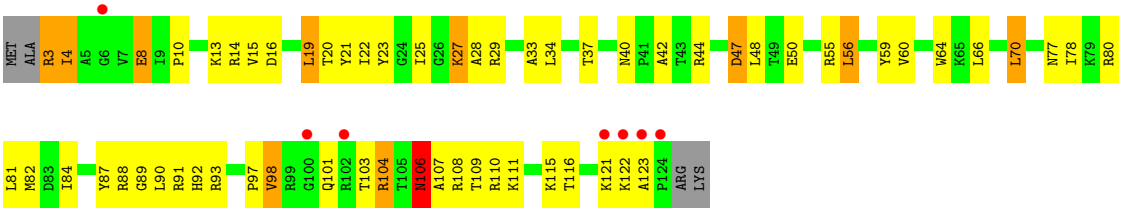
• Molecule 13: 30S Ribosomal Protein S13

Chain AM:



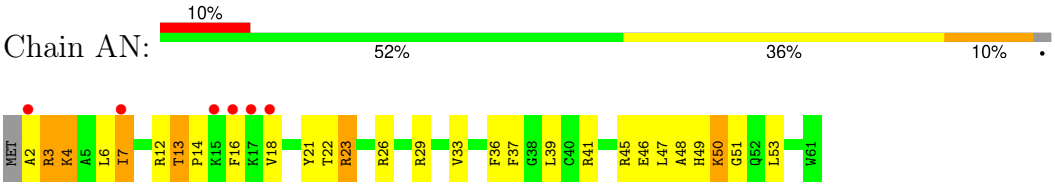
• Molecule 13: 30S Ribosomal Protein S13

Chain CM:



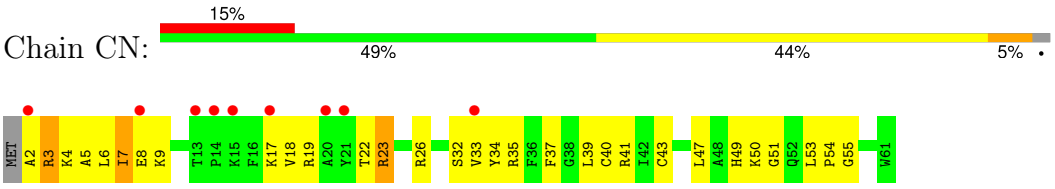
• Molecule 14: 30S Ribosomal Protein S14

Chain AN:



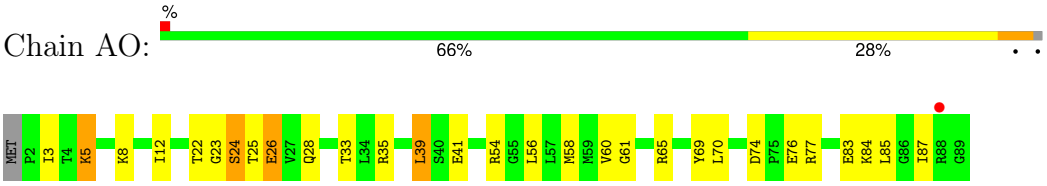
• Molecule 14: 30S Ribosomal Protein S14

Chain CN:



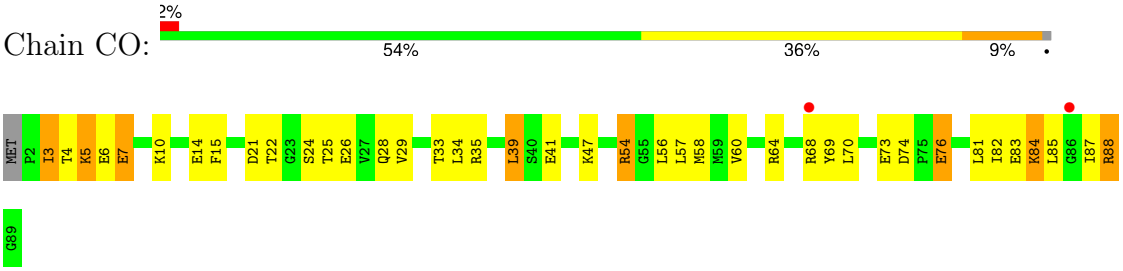
• Molecule 15: 30S Ribosomal Protein S15

Chain AO:



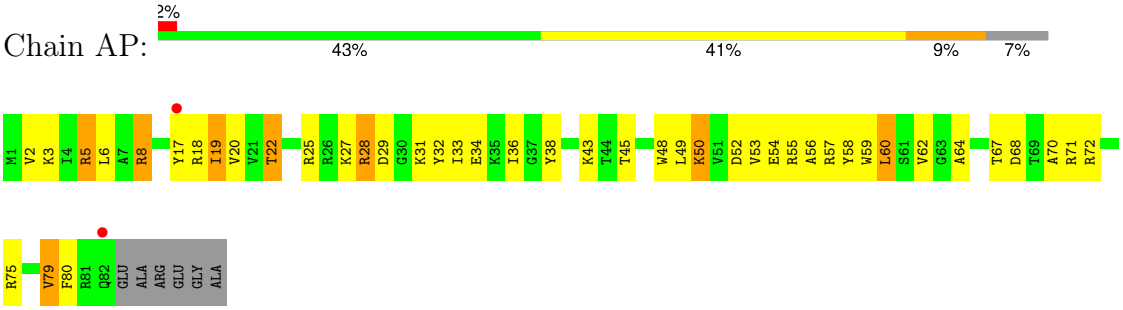
• Molecule 15: 30S Ribosomal Protein S15

Chain CO:



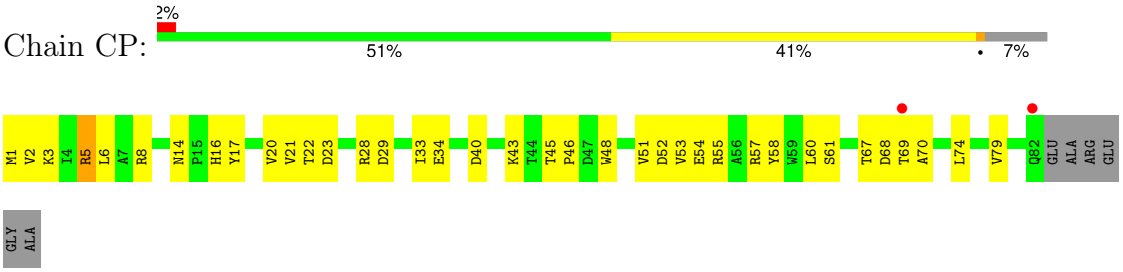
• Molecule 16: 30S Ribosomal Protein S16

Chain AP:



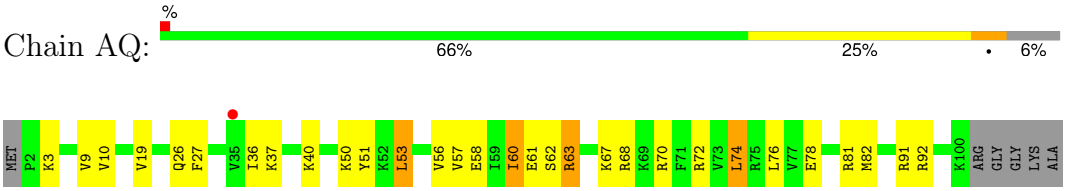
• Molecule 16: 30S Ribosomal Protein S16

Chain CP:



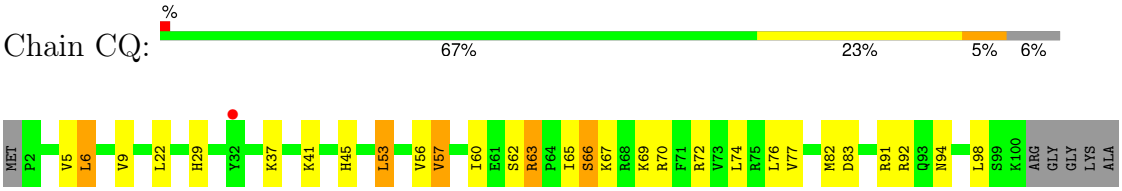
• Molecule 17: 30S Ribosomal Protein S17

Chain AQ:



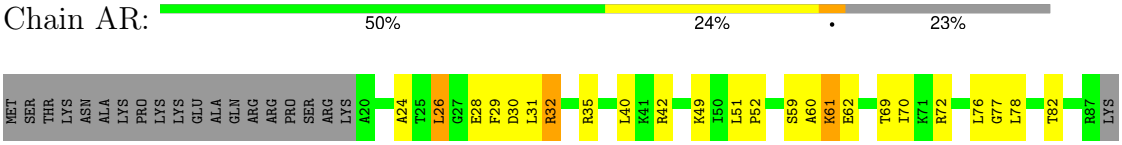
• Molecule 17: 30S Ribosomal Protein S17

Chain CQ:



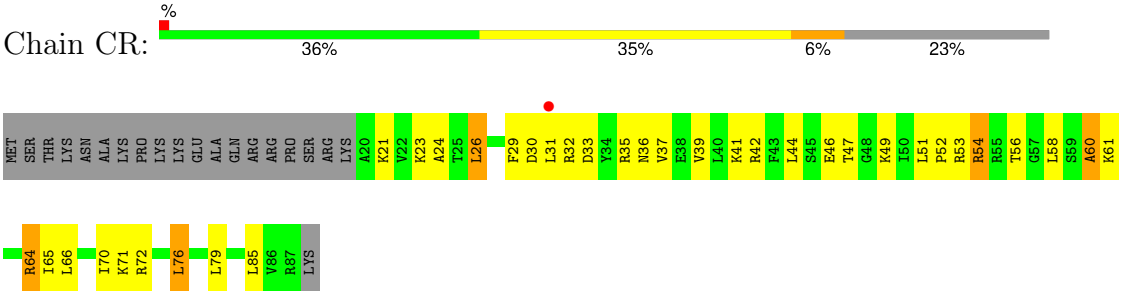
• Molecule 18: 30S Ribosomal Protein S18

Chain AR:



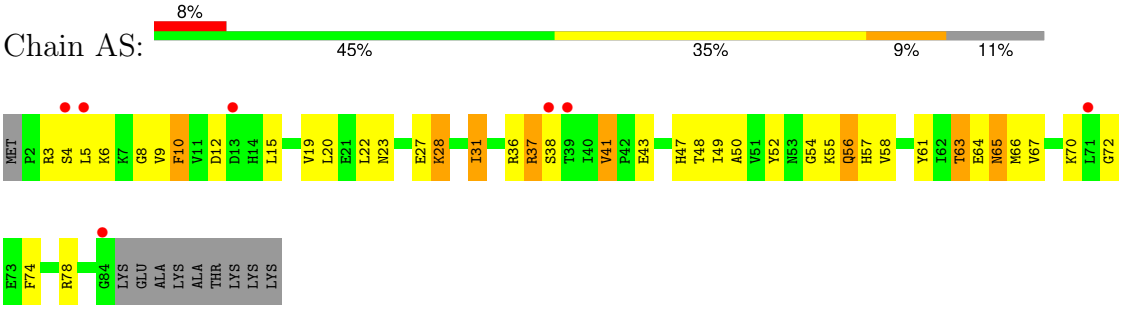
• Molecule 18: 30S Ribosomal Protein S18

Chain CR:



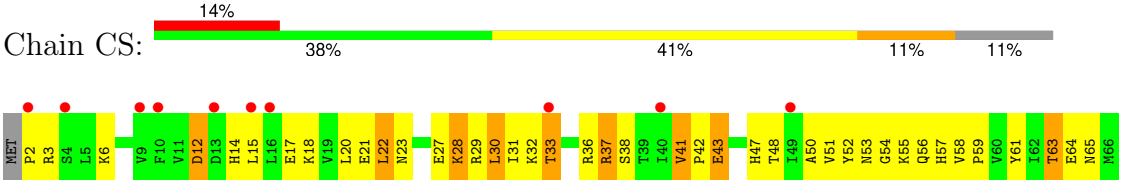
• Molecule 19: 30S Ribosomal Protein S19

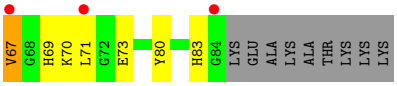
Chain AS:



• Molecule 19: 30S Ribosomal Protein S19

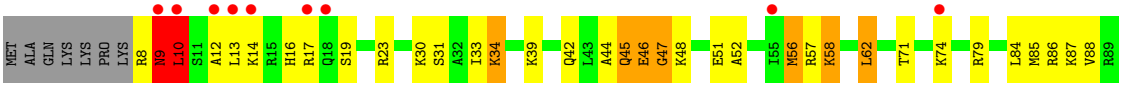
Chain CS:

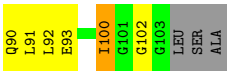




• Molecule 20: 30S Ribosomal Protein S20

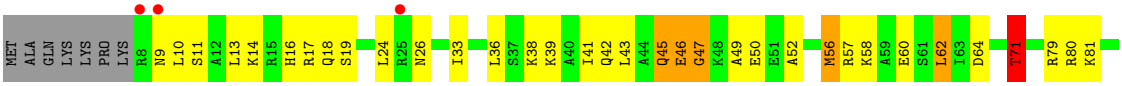
Chain AT:

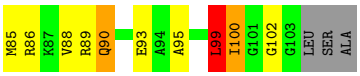




• Molecule 20: 30S Ribosomal Protein S20

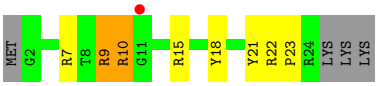
Chain CT:





• Molecule 21: 30S Ribosomal Protein THX

Chain AU:

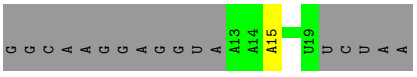


• Molecule 21: 30S Ribosomal Protein THX

Chain CU:

• Molecule 22: mRNA

Chain AV:

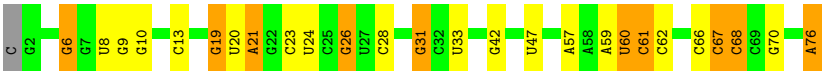


• Molecule 22: mRNA

Chain CV:

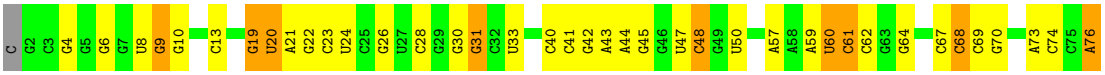
• Molecule 23: P-site tRNA

Chain AX:



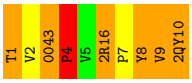
• Molecule 23: P-site tRNA

Chain CX:



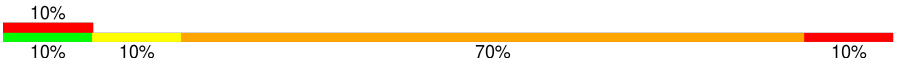
• Molecule 24: GE82832

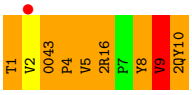
Chain AW:



• Molecule 24: GE82832

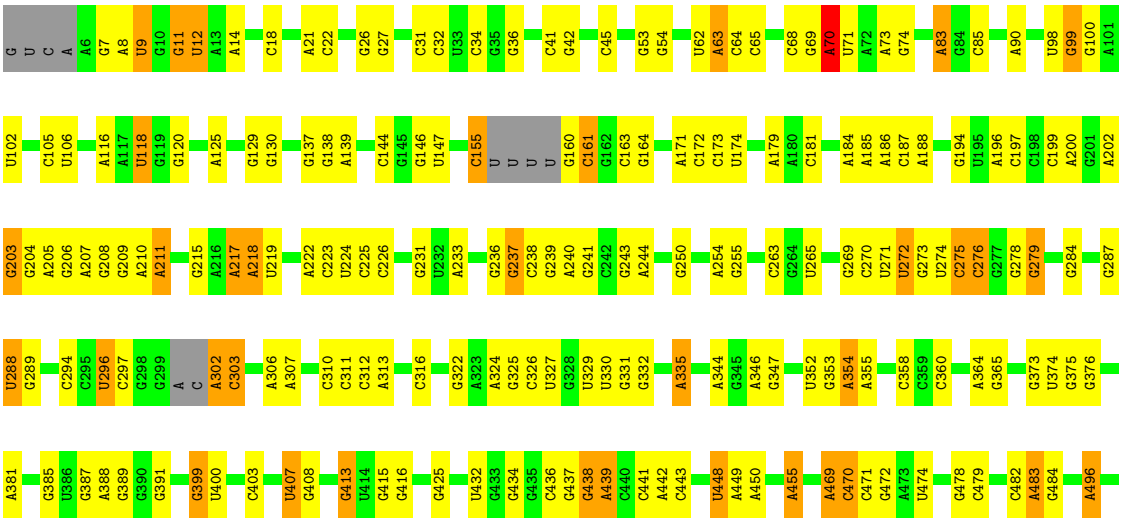
Chain CW:

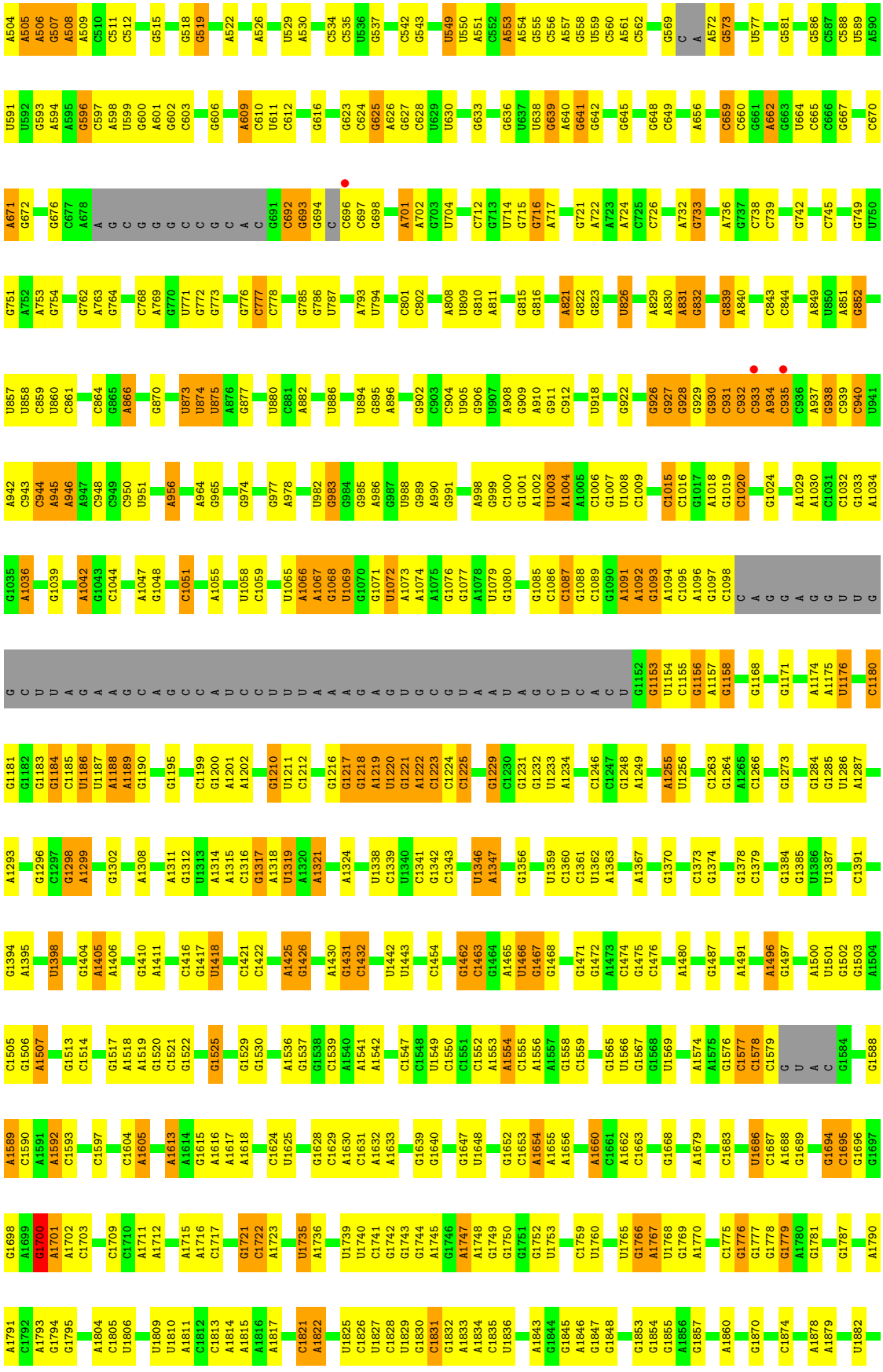


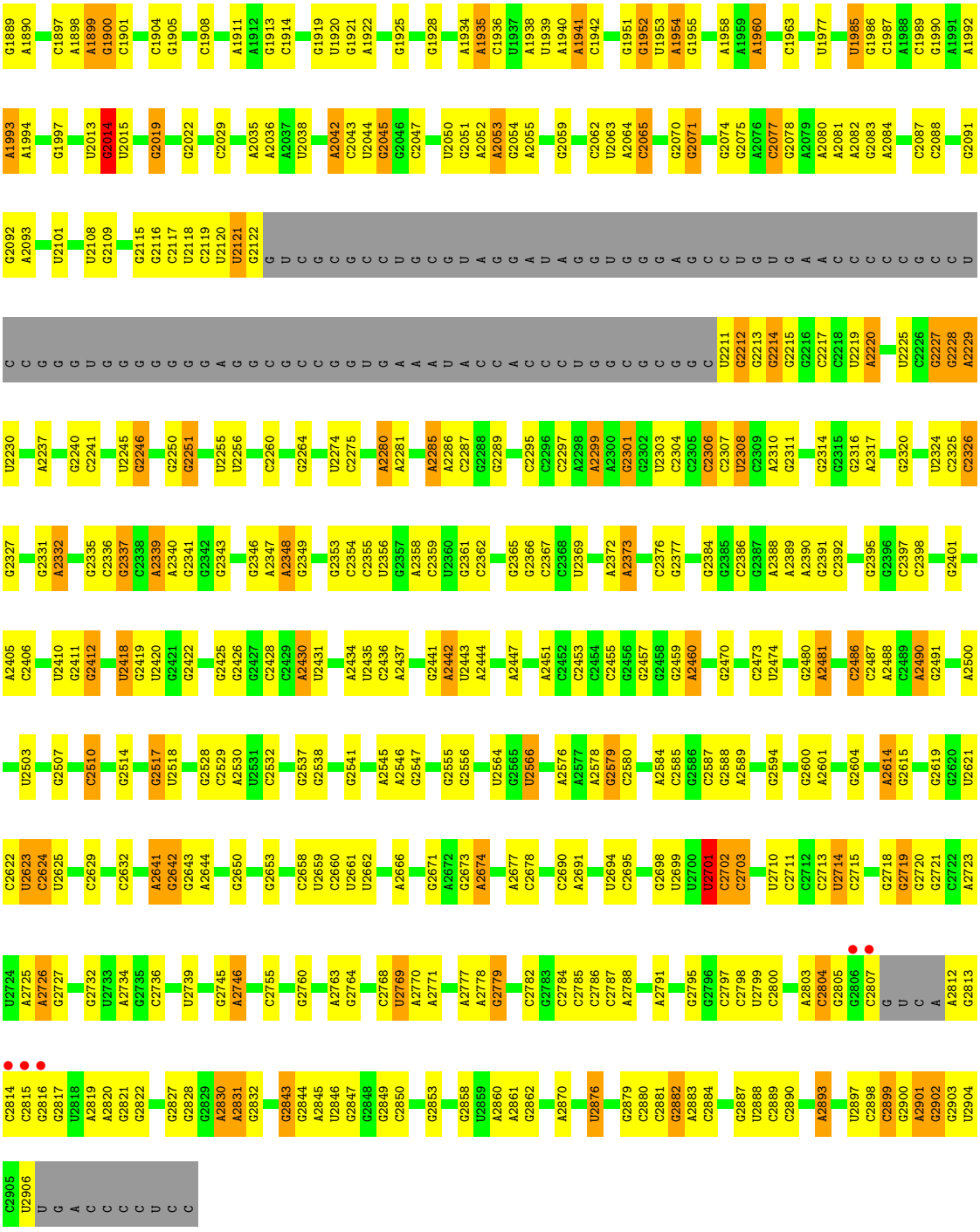


• Molecule 25: 23S Ribosomal RNA

Chain BA:

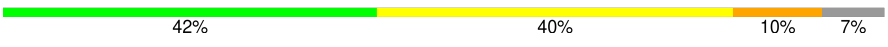


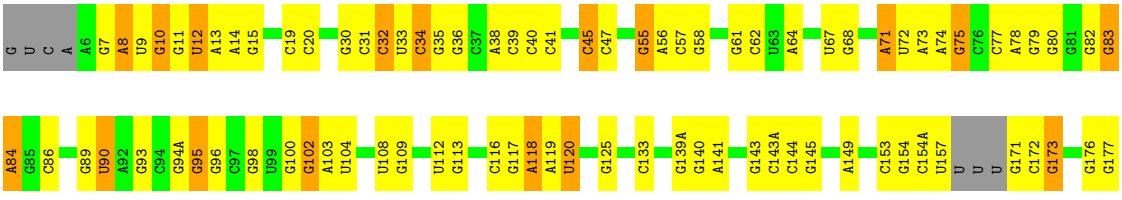


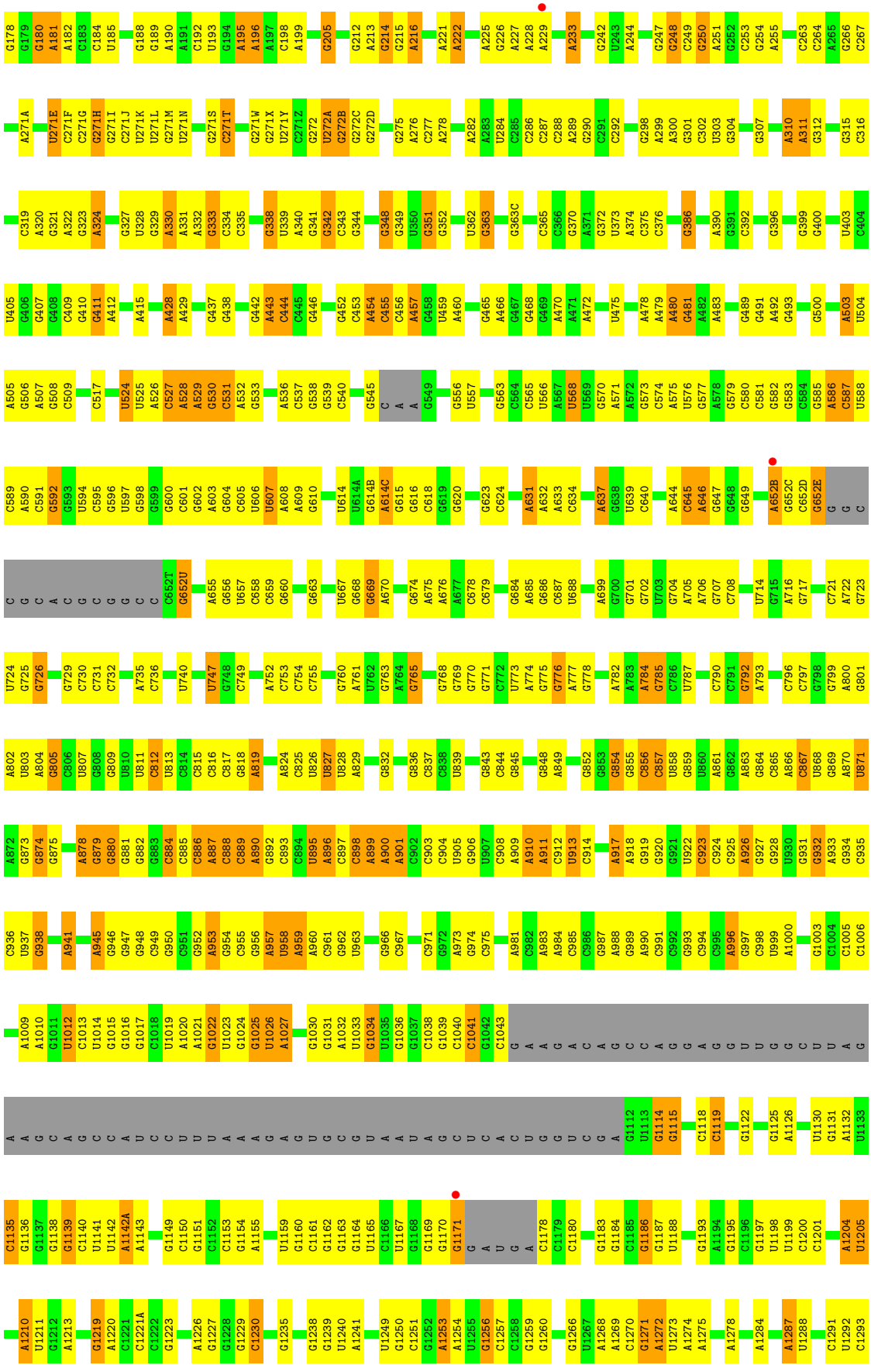


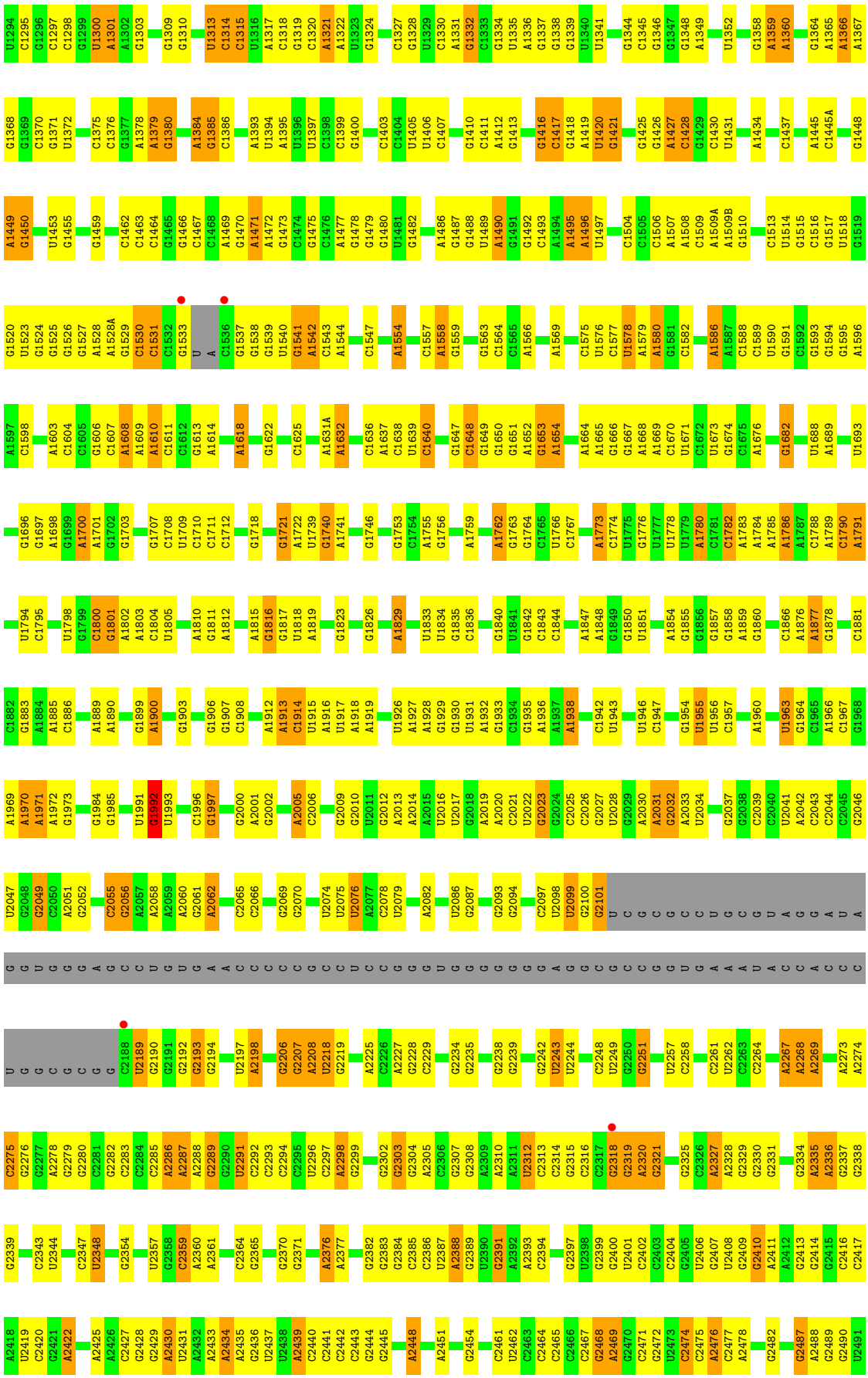
• Molecule 25: 23S Ribosomal RNA

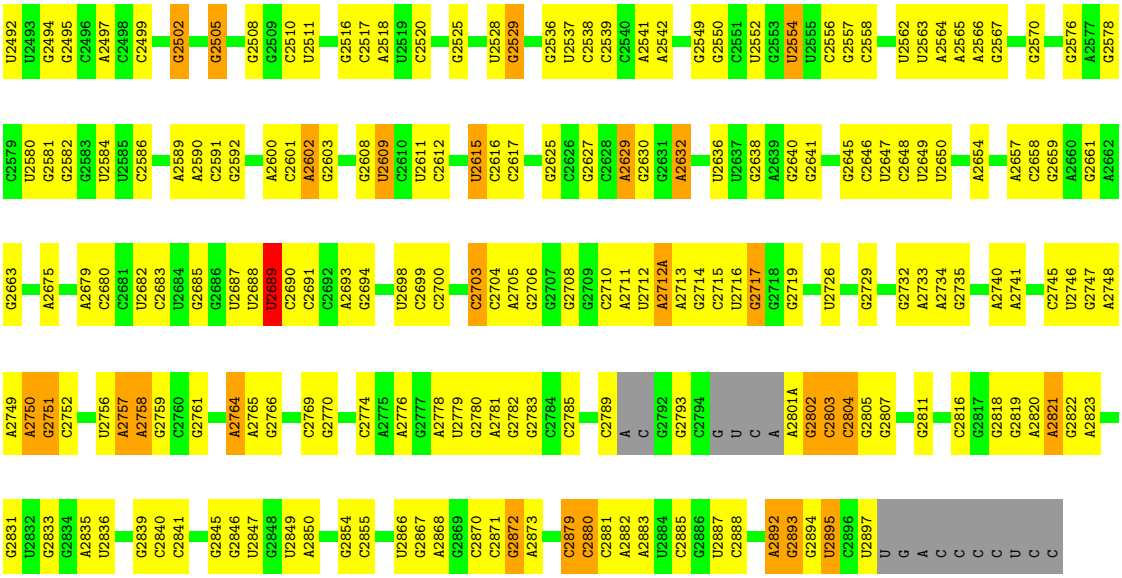
Chain DA:





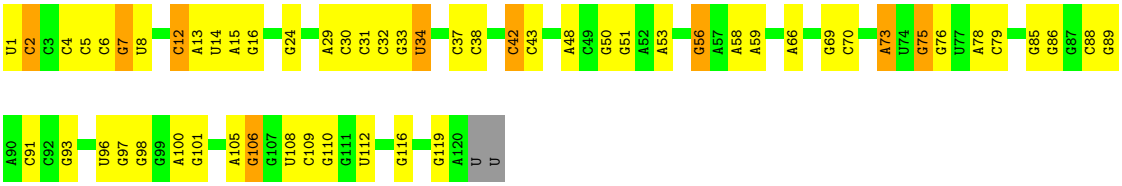






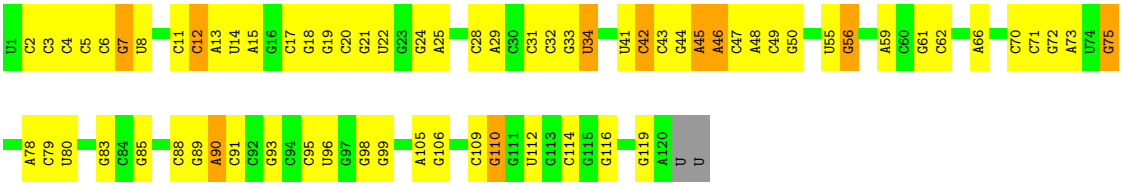
• Molecule 26: 5S Ribosomal RNA

Chain BB:



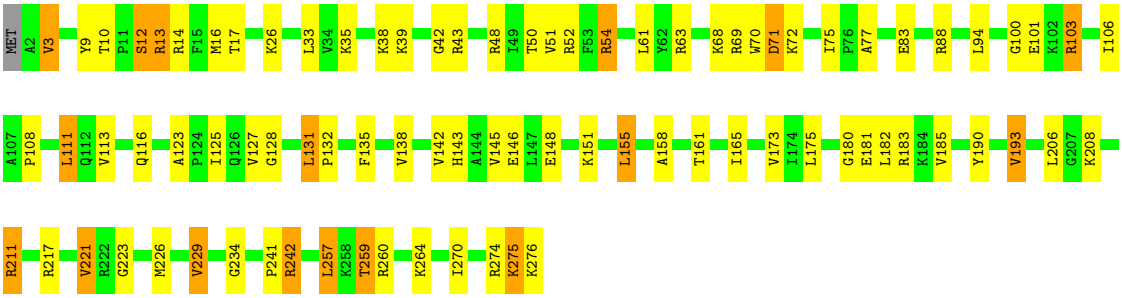
• Molecule 26: 5S Ribosomal RNA

Chain DB:



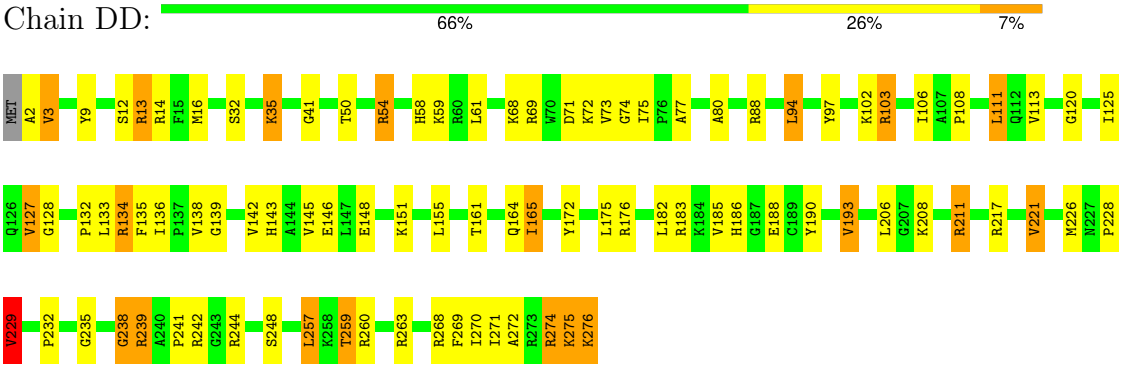
• Molecule 27: 50S Ribosomal Protein L2

Chain BD:



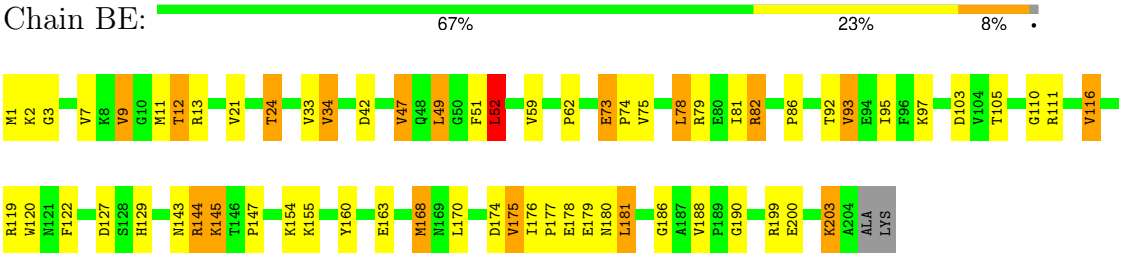
• Molecule 27: 50S Ribosomal Protein L2

Chain DD:



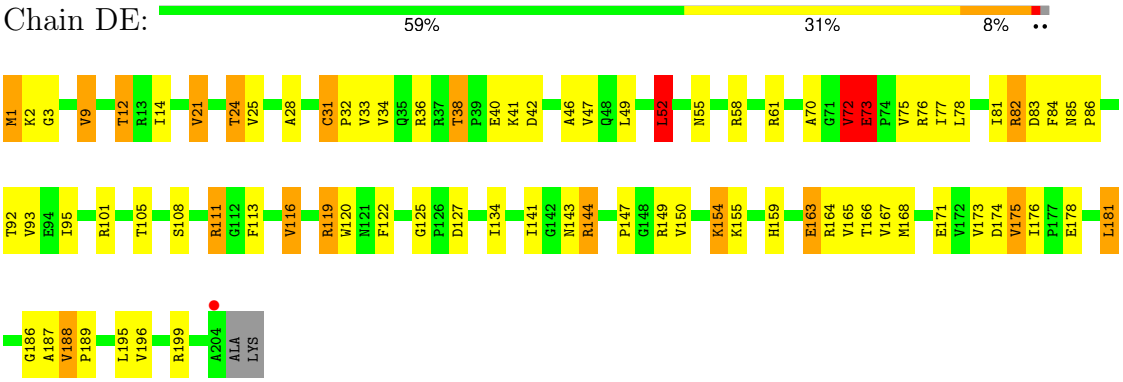
• Molecule 28: 50S Ribosomal Protein L3

Chain BE:



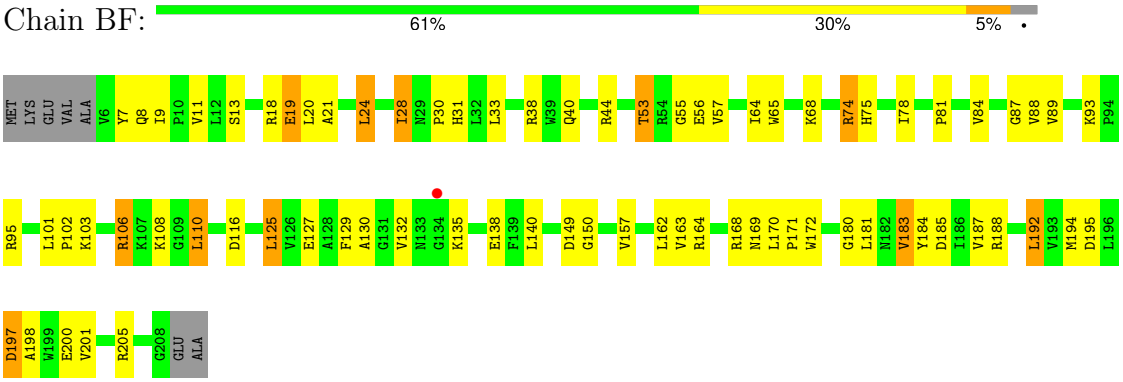
• Molecule 28: 50S Ribosomal Protein L3

Chain DE:



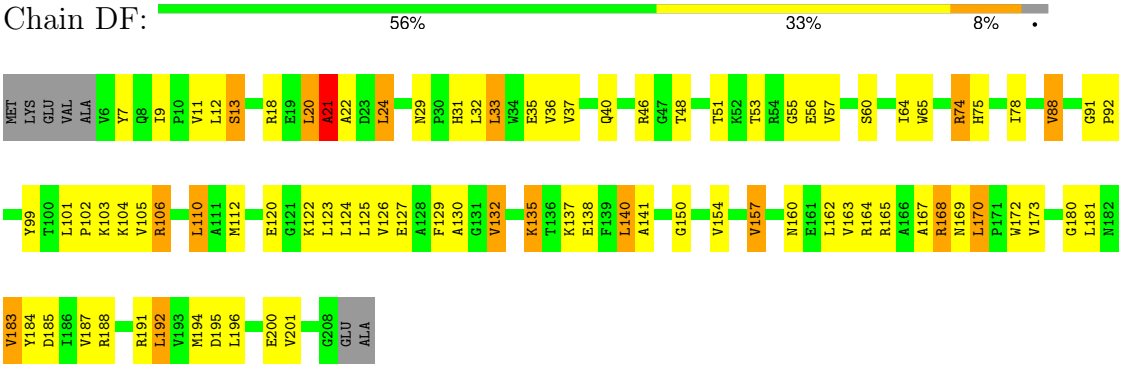
• Molecule 29: 50S Ribosomal Protein L4

Chain BF:



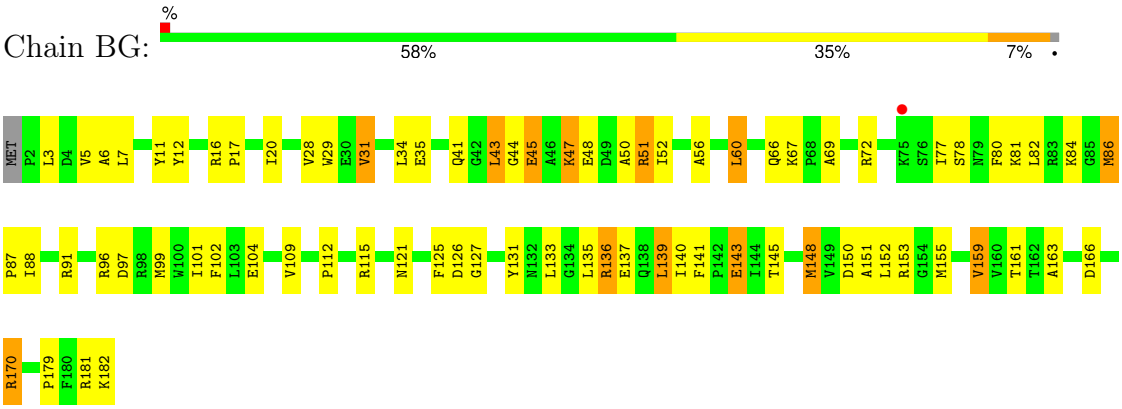
• Molecule 29: 50S Ribosomal Protein L4

Chain DF:



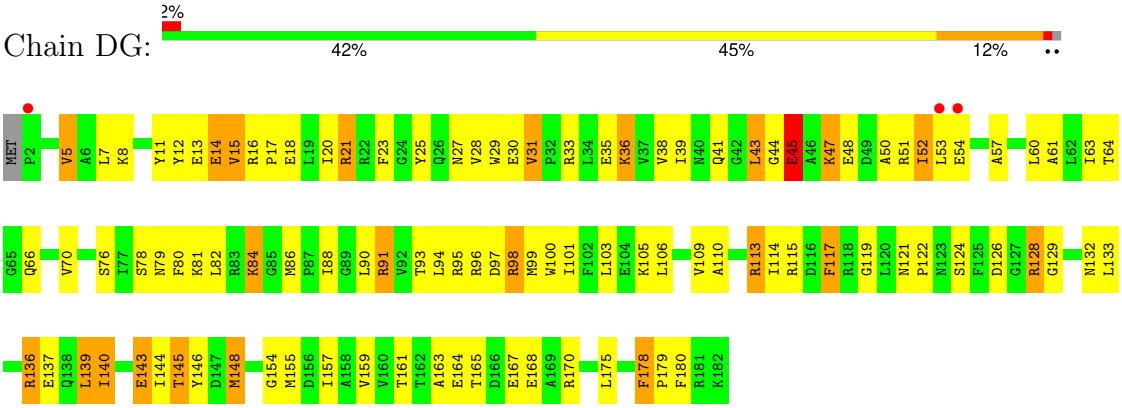
• Molecule 30: 50S Ribosomal Protein L5

Chain BG:



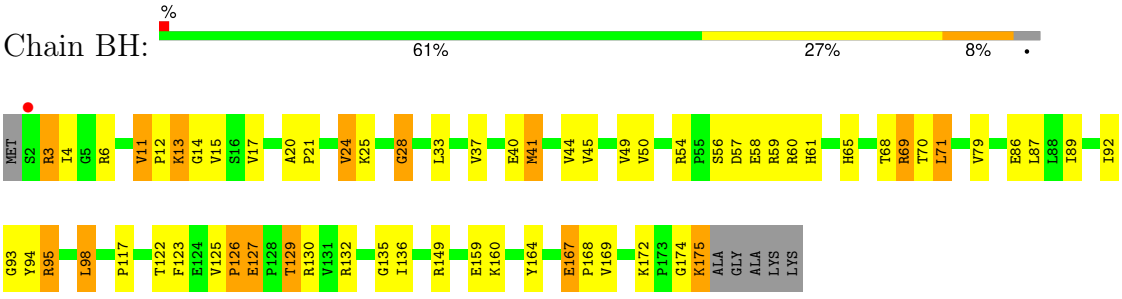
• Molecule 30: 50S Ribosomal Protein L5

Chain DG:



• Molecule 31: 50S Ribosomal Protein L6

Chain BH:

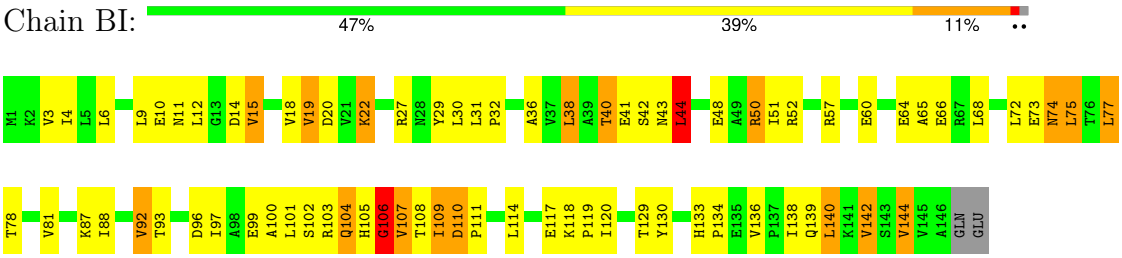


• Molecule 31: 50S Ribosomal Protein L6

Chain DH:

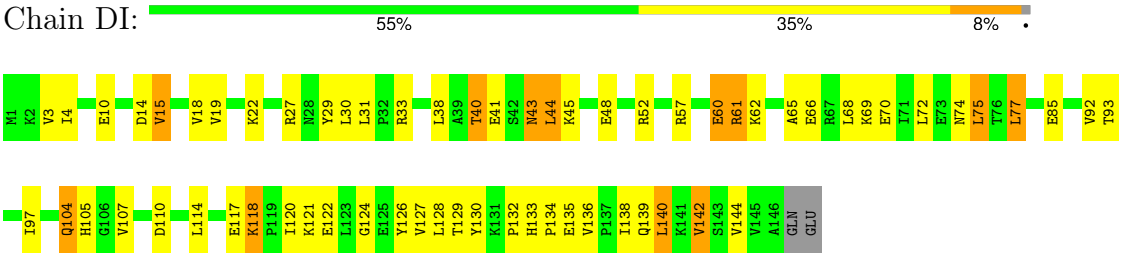
• Molecule 32: 50S Ribosomal Protein L9

Chain BI:



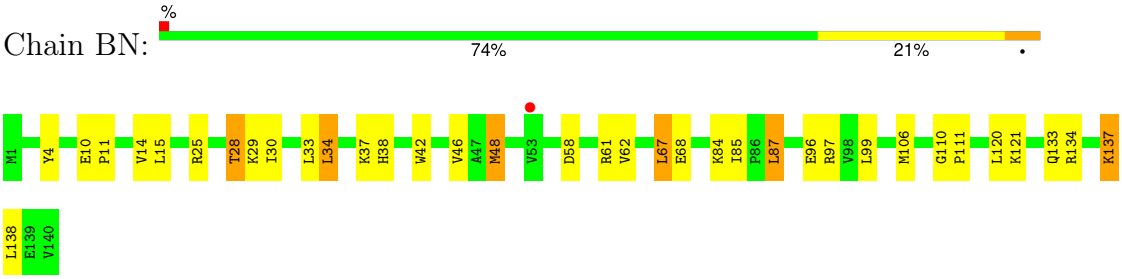
• Molecule 32: 50S Ribosomal Protein L9

Chain DI:



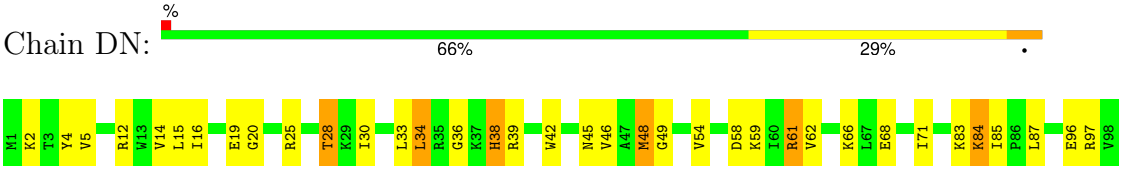
• Molecule 33: 50S Ribosomal Protein L13

Chain BN:



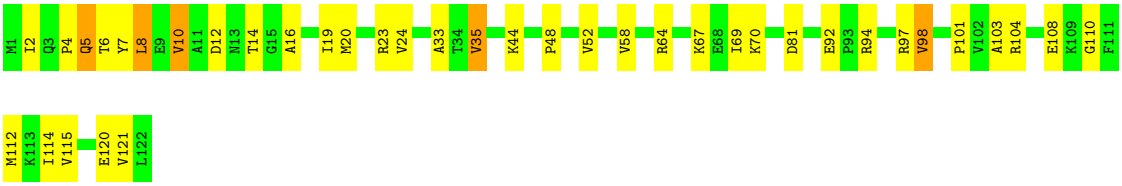
• Molecule 33: 50S Ribosomal Protein L13

Chain DN:



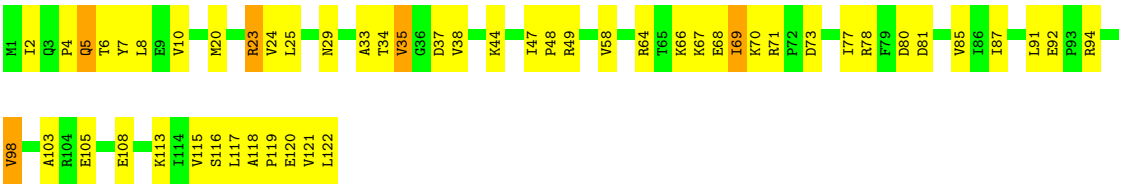
• Molecule 34: 50S Ribosomal Protein L14

Chain BO:



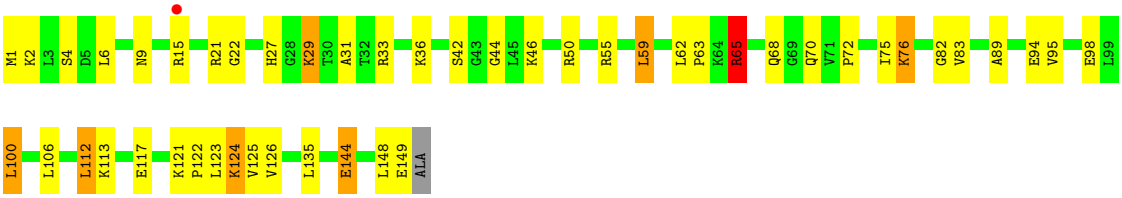
• Molecule 34: 50S Ribosomal Protein L14

Chain DO:



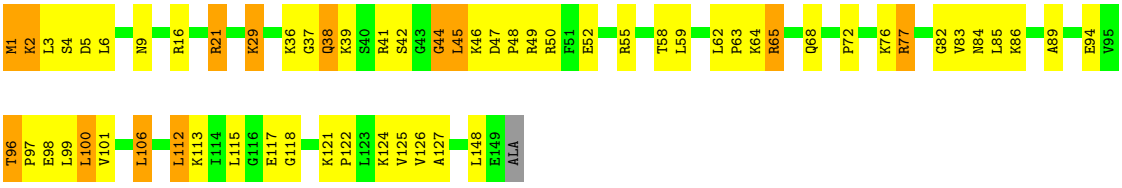
• Molecule 35: 50S Ribosomal Protein L15

Chain BP:



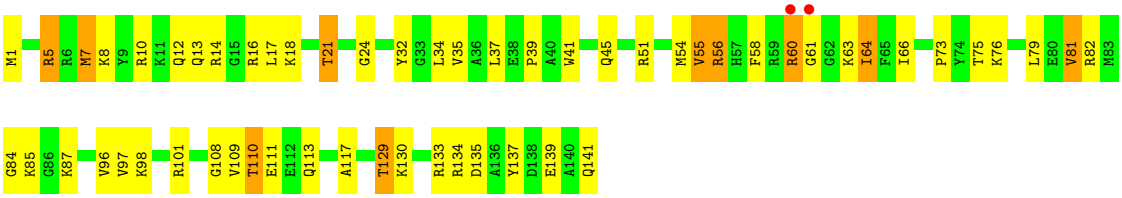
• Molecule 35: 50S Ribosomal Protein L15

Chain DP:



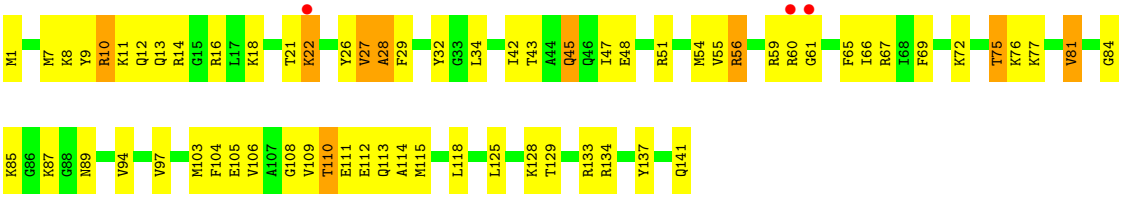
• Molecule 36: 50S Ribosomal Protein L16

Chain BQ:



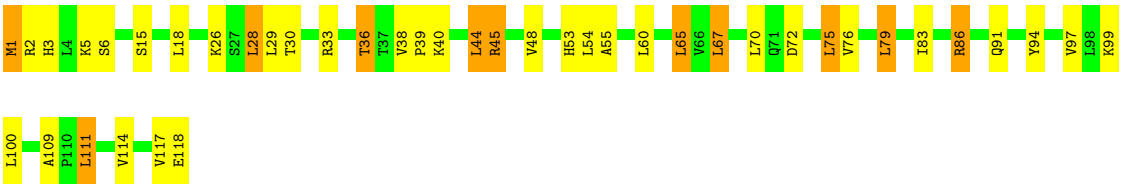
- Molecule 36: 50S Ribosomal Protein L16

Chain DQ:



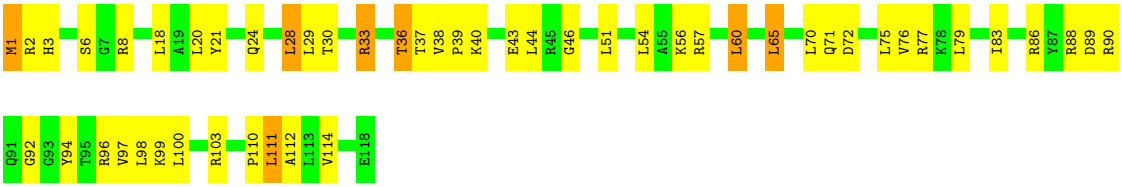
- Molecule 37: 50S Ribosomal Protein L17

Chain BR:



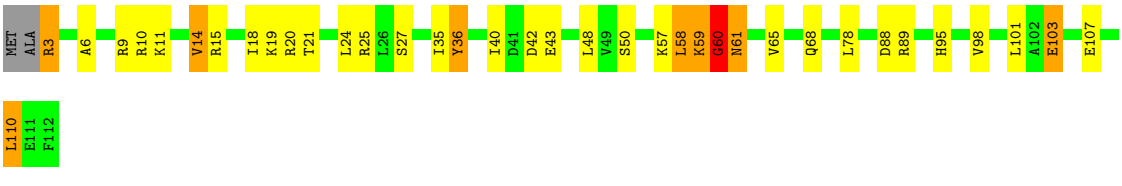
- Molecule 37: 50S Ribosomal Protein L17

Chain DR:



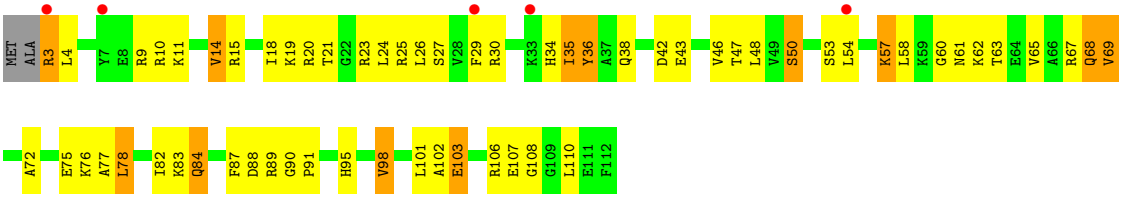
- Molecule 38: 50S Ribosomal Protein L18

Chain BS:



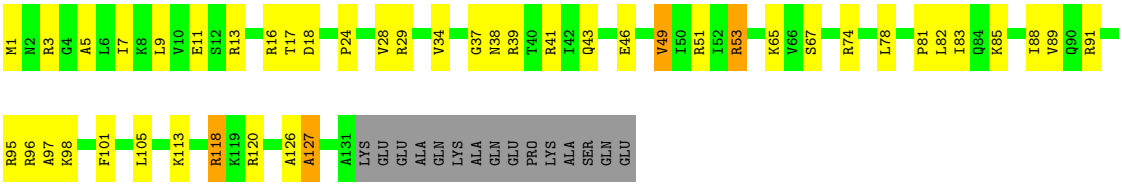
- Molecule 38: 50S Ribosomal Protein L18

Chain DS:



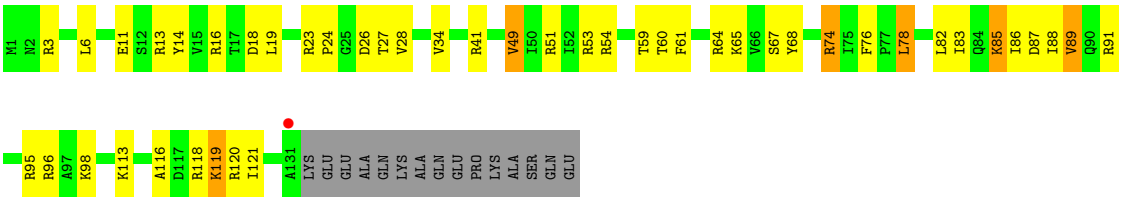
• Molecule 39: 50S Ribosomal Protein L19

Chain BT:



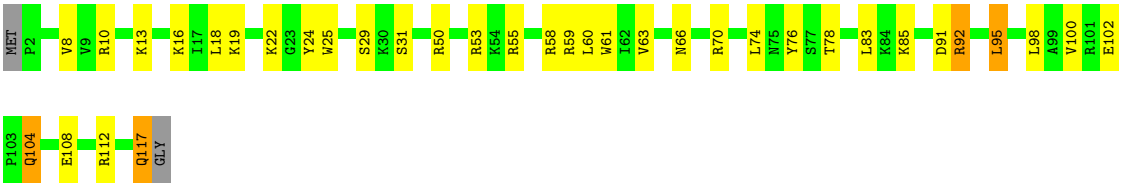
• Molecule 39: 50S Ribosomal Protein L19

Chain DT:



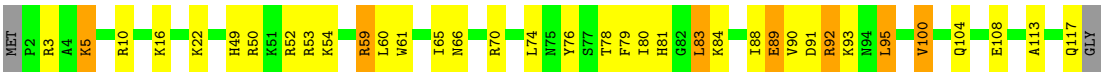
• Molecule 40: 50S Ribosomal Protein L20

Chain BU:



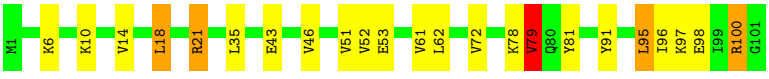
• Molecule 40: 50S Ribosomal Protein L20

Chain DU:



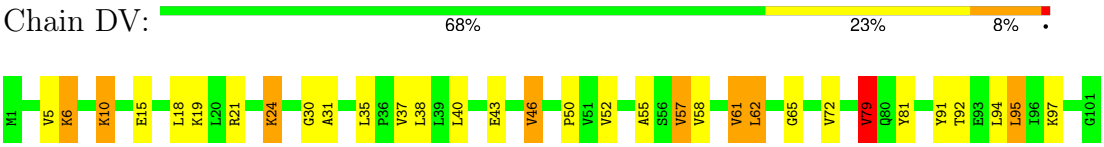
• Molecule 41: 50S Ribosomal Protein L21

Chain BV:



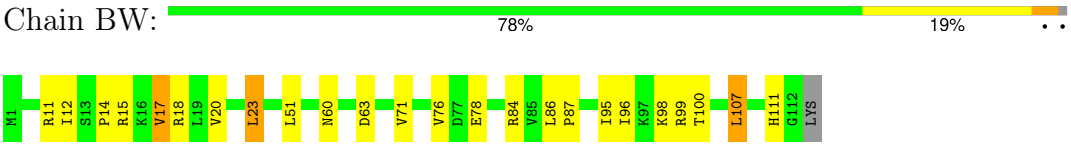
• Molecule 41: 50S Ribosomal Protein L21

Chain DV:



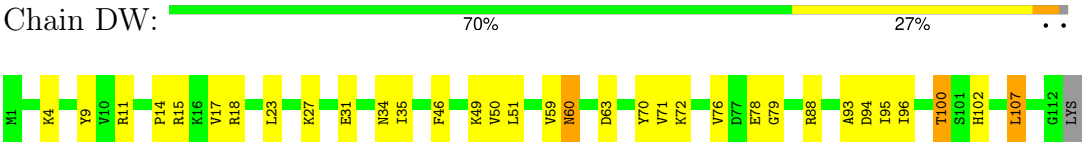
• Molecule 42: 50S Ribosomal Protein L22

Chain BW:



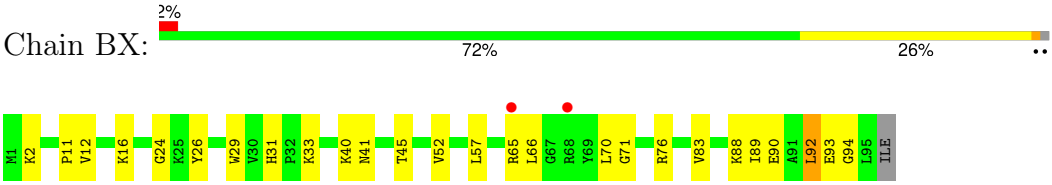
• Molecule 42: 50S Ribosomal Protein L22

Chain DW:



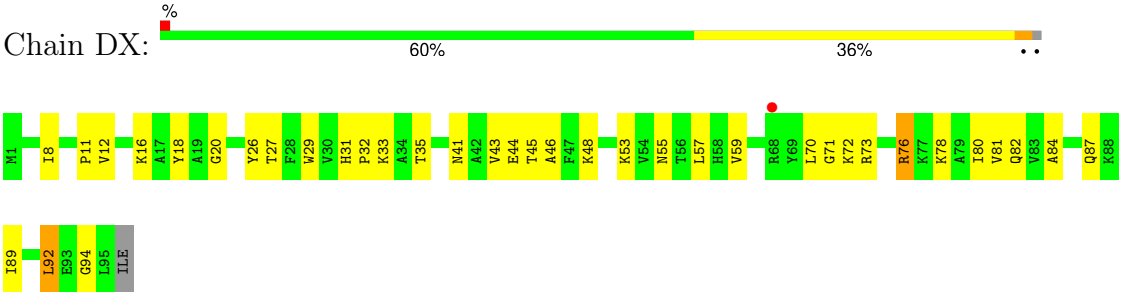
• Molecule 43: 50S Ribosomal Protein L23

Chain BX:



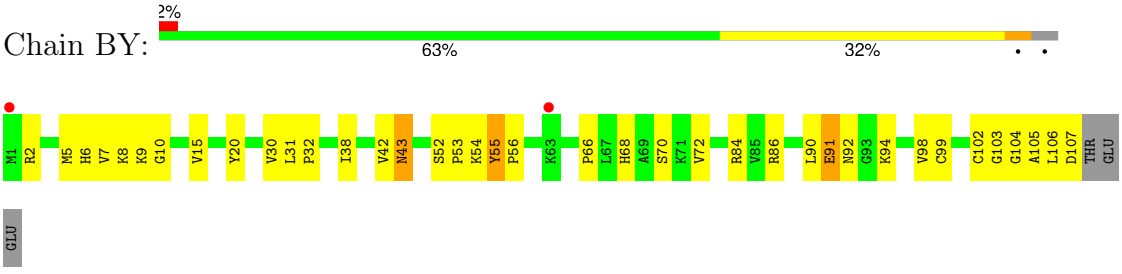
• Molecule 43: 50S Ribosomal Protein L23

Chain DX:



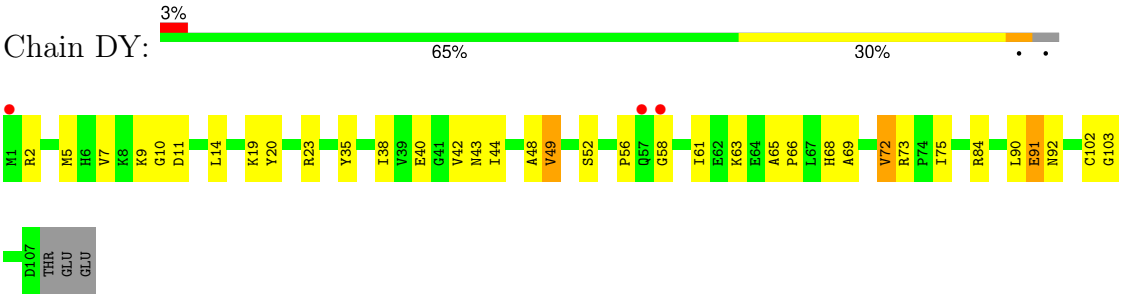
• Molecule 44: 50S Ribosomal Protein L24

Chain BY:



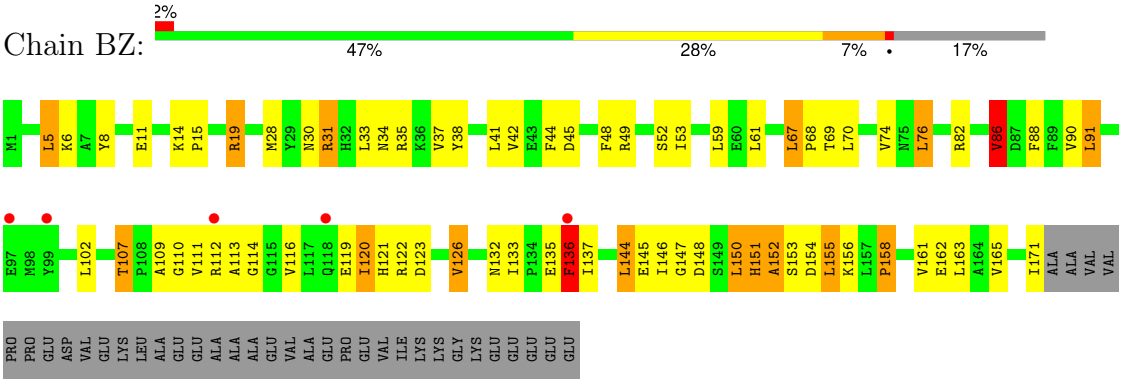
• Molecule 44: 50S Ribosomal Protein L24

Chain DY:



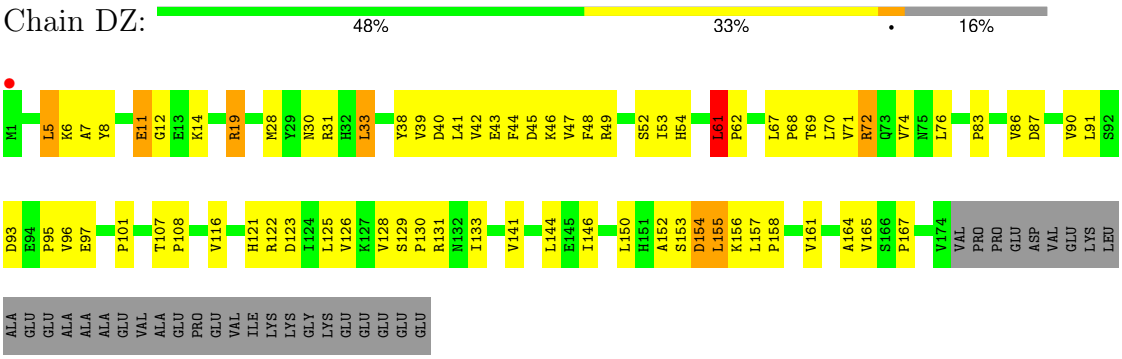
• Molecule 45: 50S Ribosomal Protein L25

Chain BZ:



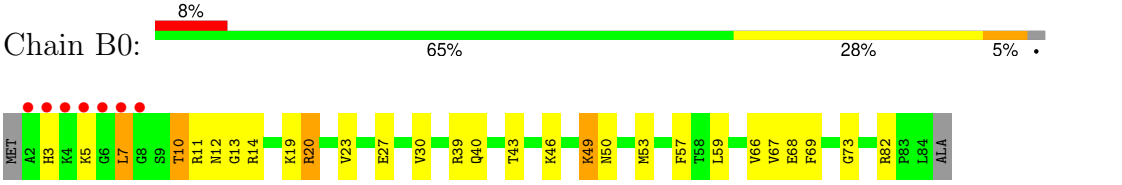
• Molecule 45: 50S Ribosomal Protein L25

Chain DZ:



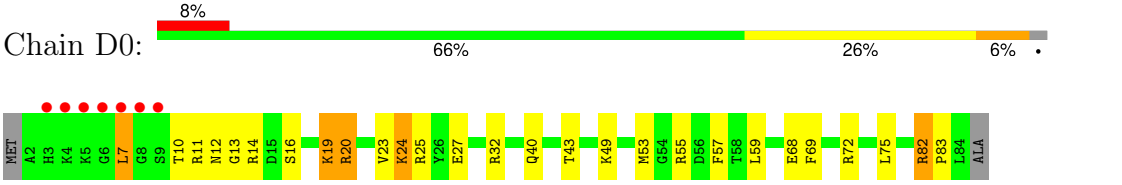
• Molecule 46: 50S Ribosomal Protein L27

Chain B0:



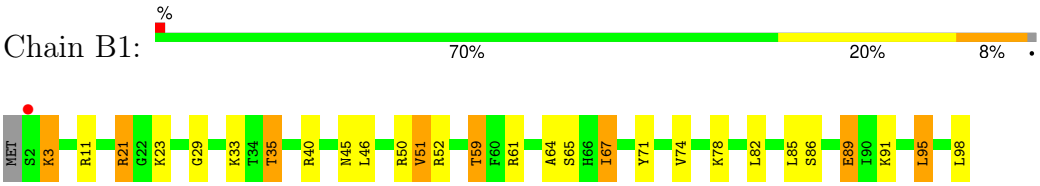
• Molecule 46: 50S Ribosomal Protein L27

Chain D0:



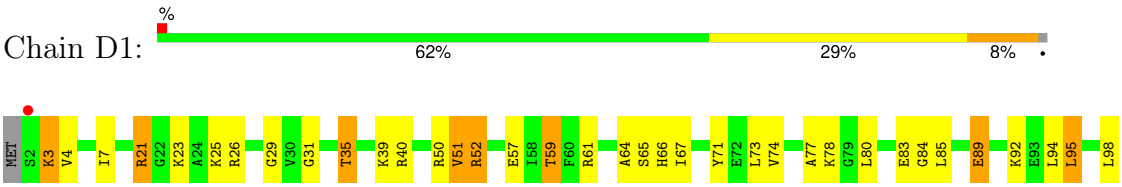
• Molecule 47: 50S Ribosomal Protein L28

Chain B1:



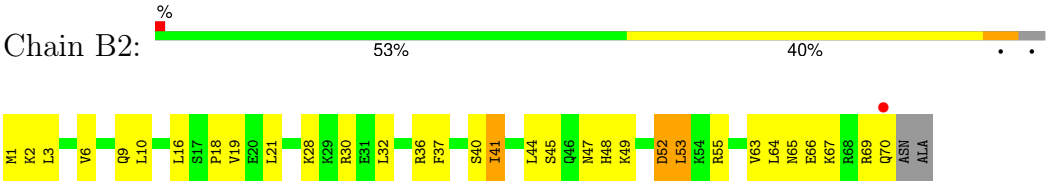
• Molecule 47: 50S Ribosomal Protein L28

Chain D1:



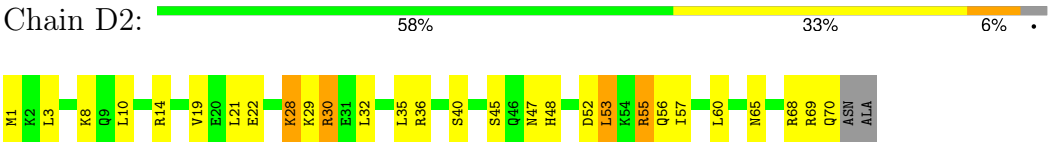
• Molecule 48: 50S Ribosomal Protein L29

Chain B2:



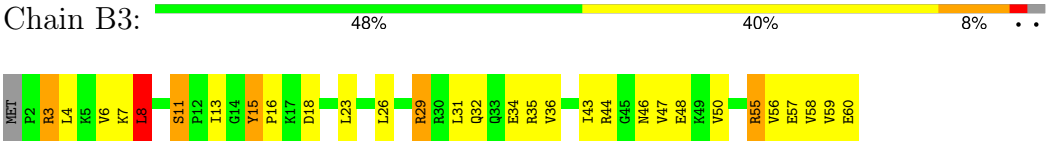
• Molecule 48: 50S Ribosomal Protein L29

Chain D2:



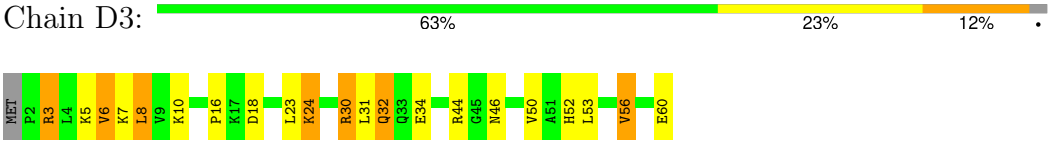
• Molecule 49: 50S Ribosomal Protein L30

Chain B3:



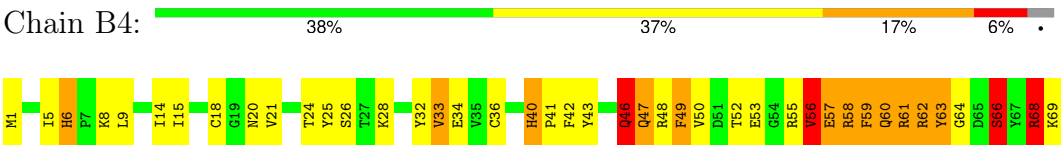
• Molecule 49: 50S Ribosomal Protein L30

Chain D3:



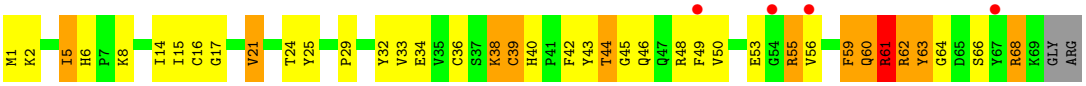
• Molecule 50: 50S Ribosomal Protein L31

Chain B4:



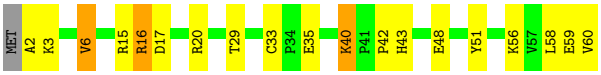
• Molecule 50: 50S Ribosomal Protein L31

Chain D4:



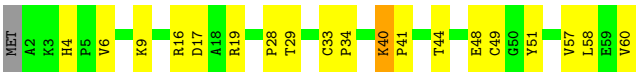
• Molecule 51: 50S Ribosomal Protein L32

Chain B5:



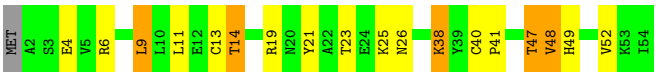
• Molecule 51: 50S Ribosomal Protein L32

Chain D5:



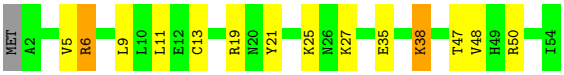
• Molecule 52: 50S Ribosomal Protein L33

Chain B6:



• Molecule 52: 50S Ribosomal Protein L33

Chain D6:



• Molecule 53: 50S Ribosomal Protein L34

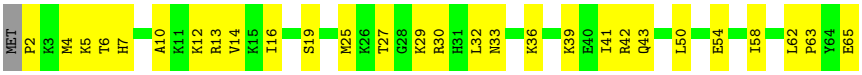
Chain B7:

• Molecule 53: 50S Ribosomal Protein L34

Chain D7:

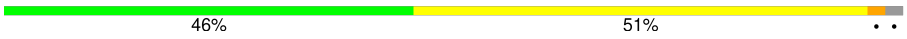
• Molecule 54: 50S Ribosomal Protein L35

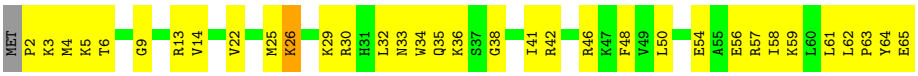
Chain B8:



• Molecule 54: 50S Ribosomal Protein L35

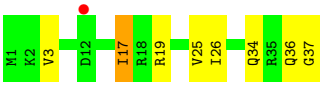
Chain D8:





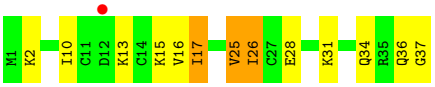
• Molecule 55: 50S Ribosomal Protein L36

Chain B9:



• Molecule 55: 50S Ribosomal Protein L36

Chain D9:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.68Å 450.64Å 622.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.68 – 3.10 49.68 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.2 (49.68-3.10) 98.1 (49.68-3.10)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	0.25	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.203 , 0.260 0.203 , 0.258	Depositor DCC
R_{free} test set	51894 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	71.0	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 55.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	286321	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MVA, 2QY, MG, 2R3, 004, ZN, K, 2R1, SF4, 2QZ, FME

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	AA	0.41	0/36038	0.64	2/56244 (0.0%)
1	CA	0.41	0/36170	0.64	11/56452 (0.0%)
2	AB	0.62	1/1881 (0.1%)	1.19	19/2542 (0.7%)
2	CB	0.70	1/1860 (0.1%)	1.18	15/2518 (0.6%)
3	AC	0.62	0/1576	1.01	2/2130 (0.1%)
3	CC	0.65	0/1566	1.09	7/2119 (0.3%)
4	AD	0.64	0/1689	1.12	10/2267 (0.4%)
4	CD	0.61	0/1704	1.08	12/2284 (0.5%)
5	AE	0.63	0/1145	1.11	9/1543 (0.6%)
5	CE	0.62	0/1149	1.17	11/1548 (0.7%)
6	AF	0.58	0/819	0.99	1/1111 (0.1%)
6	CF	0.64	0/829	1.03	2/1123 (0.2%)
7	AG	0.62	0/1250	1.05	4/1679 (0.2%)
7	CG	0.61	0/1254	1.09	4/1683 (0.2%)
8	AH	0.58	0/1108	1.03	4/1494 (0.3%)
8	CH	0.57	0/1108	1.08	3/1494 (0.2%)
9	AI	0.59	0/1002	1.05	3/1346 (0.2%)
9	CI	0.72	0/997	1.09	5/1343 (0.4%)
10	AJ	0.69	0/722	1.15	4/982 (0.4%)
10	CJ	0.72	0/727	1.10	5/988 (0.5%)
11	AK	0.59	0/844	1.03	1/1145 (0.1%)
11	CK	0.58	0/848	0.99	1/1149 (0.1%)
12	AL	0.65	0/946	1.04	5/1274 (0.4%)
12	CL	0.63	0/946	1.02	3/1274 (0.2%)
13	AM	0.56	0/969	1.04	2/1302 (0.2%)
13	CM	0.64	0/961	1.05	4/1291 (0.3%)
14	AN	0.56	0/501	1.02	2/664 (0.3%)
14	CN	0.65	0/501	1.03	0/664
15	AO	0.61	0/739	1.03	1/985 (0.1%)
15	CO	0.57	0/739	1.06	3/985 (0.3%)
16	AP	0.62	0/697	1.08	4/939 (0.4%)
16	CP	0.61	0/693	1.01	2/935 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.57	0/836	0.93	0/1117
17	CQ	0.55	0/836	1.00	3/1117 (0.3%)
18	AR	0.63	0/560	0.96	1/746 (0.1%)
18	CR	0.61	0/560	0.96	0/746
19	AS	0.64	0/667	1.09	3/900 (0.3%)
19	CS	0.72	0/661	1.16	1/893 (0.1%)
20	AT	0.62	0/730	1.18	2/965 (0.2%)
20	CT	0.58	0/729	1.04	1/965 (0.1%)
21	AU	0.56	0/203	0.98	0/266
21	CU	0.63	0/203	1.07	0/266
22	AV	0.51	0/127	0.72	0/198
22	CV	0.53	0/126	0.68	0/195
23	AX	0.41	0/1813	0.63	1/2825 (0.0%)
23	CX	0.44	0/1813	0.76	1/2825 (0.0%)
24	AW	0.47	0/20	0.84	0/23
24	CW	0.39	0/20	0.67	0/23
25	BA	0.57	0/65892	0.68	10/102850 (0.0%)
25	DA	0.43	0/65466	0.65	2/102184 (0.0%)
26	BB	0.45	0/2878	0.60	0/4490
26	DB	0.47	0/2878	0.67	0/4490
27	BD	0.87	0/2186	1.12	7/2944 (0.2%)
27	DD	0.75	0/2186	1.11	9/2944 (0.3%)
28	BE	0.91	0/1592	1.14	7/2149 (0.3%)
28	DE	0.71	0/1592	1.22	17/2149 (0.8%)
29	BF	0.90	1/1619 (0.1%)	1.09	3/2193 (0.1%)
29	DF	0.63	0/1615	1.12	7/2188 (0.3%)
30	BG	0.62	0/1450	1.06	5/1959 (0.3%)
30	DG	0.68	0/1449	1.18	8/1958 (0.4%)
31	BH	0.80	0/1356	1.14	14/1834 (0.8%)
31	DH	0.69	0/1356	1.09	3/1834 (0.2%)
32	BI	0.67	0/1100	1.10	11/1501 (0.7%)
32	DI	0.63	0/1076	1.15	7/1471 (0.5%)
33	BN	0.87	1/1144 (0.1%)	1.06	4/1543 (0.3%)
33	DN	0.64	0/1144	1.11	4/1543 (0.3%)
34	BO	0.84	0/943	1.08	0/1269
34	DO	0.70	0/943	1.04	0/1269
35	BP	0.84	0/1152	1.07	5/1533 (0.3%)
35	DP	0.62	0/1152	1.11	4/1533 (0.3%)
36	BQ	0.85	0/1143	1.09	3/1527 (0.2%)
36	DQ	0.73	0/1143	1.11	3/1527 (0.2%)
37	BR	0.84	0/982	0.99	0/1312
37	DR	0.66	0/982	0.93	0/1312
38	BS	0.68	0/887	1.06	2/1180 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	DS	0.59	0/880	1.06	1/1172 (0.1%)
39	BT	0.80	0/1105	1.07	0/1477
39	DT	0.62	0/1097	1.04	1/1468 (0.1%)
40	BU	0.91	0/977	1.02	3/1301 (0.2%)
40	DU	0.69	0/977	0.98	0/1301
41	BV	0.87	0/782	1.09	3/1049 (0.3%)
41	DV	0.66	0/782	1.00	1/1049 (0.1%)
42	BW	1.03	0/897	1.06	1/1205 (0.1%)
42	DW	0.72	0/897	1.08	0/1205
43	BX	0.85	0/764	1.06	2/1025 (0.2%)
43	DX	0.65	0/764	1.05	0/1025
44	BY	0.83	0/819	1.16	6/1095 (0.5%)
44	DY	0.63	0/819	1.11	3/1095 (0.3%)
45	BZ	0.71	0/1379	1.14	10/1873 (0.5%)
45	DZ	0.64	0/1390	1.10	5/1890 (0.3%)
46	B0	0.82	0/662	1.14	3/881 (0.3%)
46	D0	0.65	0/662	1.09	4/881 (0.5%)
47	B1	0.82	1/762 (0.1%)	1.05	2/1014 (0.2%)
47	D1	0.66	0/762	1.05	0/1014
48	B2	0.78	0/590	1.13	0/781
48	D2	0.56	0/590	0.97	0/781
49	B3	0.87	0/474	1.22	6/635 (0.9%)
49	D3	0.57	0/469	0.98	0/630
50	B4	0.67	0/564	1.22	8/759 (1.1%)
50	D4	0.79	0/544	1.27	6/735 (0.8%)
51	B5	0.88	0/469	1.16	2/635 (0.3%)
51	D5	0.72	0/469	1.14	3/635 (0.5%)
52	B6	0.81	1/460 (0.2%)	0.88	0/613
52	D6	0.67	0/456	0.96	0/608
53	B7	1.02	0/426	1.00	1/561 (0.2%)
53	D7	0.78	0/426	1.01	2/561 (0.4%)
54	B8	0.96	0/519	1.00	0/684
54	D8	0.69	0/525	1.04	0/691
55	B9	0.82	0/310	1.05	0/407
55	D9	0.74	0/310	1.12	0/407
All	All	0.55	6/305966 (0.0%)	0.80	382/457396 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	3
4	CD	0	1
7	AG	0	1
23	CX	1	0
24	AW	0	1
24	CW	0	1
27	DD	0	1
38	BS	0	1
45	BZ	0	1
50	B4	0	1
All	All	1	11

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	B1	67	ILE	CA-CB	-6.43	1.50	1.54
33	BN	85	ILE	CA-CB	-6.22	1.49	1.54
29	BF	84	VAL	CA-CB	-5.75	1.47	1.54
2	CB	95	GLN	CA-C	5.53	1.55	1.52
52	B6	23	THR	CA-CB	5.41	1.61	1.53

The worst 5 of 382 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CX	76	A	O4'-C1'-N9	20.44	139.17	108.50
8	CH	73	ASP	CA-C-N	11.19	132.88	120.45
8	CH	73	ASP	C-N-CA	11.19	132.88	120.45
36	DQ	27	VAL	N-CA-C	10.38	120.28	110.53
43	BX	65	ARG	NE-CZ-NH2	9.78	128.00	119.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	CX	76	A	C1'

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide
2	AB	8	LYS	Peptide
2	AB	9	GLU	Peptide
7	AG	79	ARG	Peptide
24	AW	4	PRO	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32196	0	16251	813	0
1	CA	32312	0	16307	923	0
2	AB	1846	0	1867	112	0
2	CB	1825	0	1828	120	0
3	AC	1552	0	1546	62	0
3	CC	1542	0	1517	67	0
4	AD	1659	0	1676	101	0
4	CD	1674	0	1714	80	0
5	AE	1129	0	1185	49	0
5	CE	1133	0	1191	46	0
6	AF	806	0	793	35	0
6	CF	816	0	808	31	0
7	AG	1231	0	1238	37	0
7	CG	1235	0	1249	58	0
8	AH	1088	0	1126	48	0
8	CH	1088	0	1126	47	0
9	AI	983	0	986	56	0
9	CI	978	0	966	60	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	47	0
11	AK	829	0	825	19	0
11	CK	833	0	836	29	0
12	AL	930	0	980	30	0
12	CL	930	0	980	34	0
13	AM	958	0	1002	28	0
13	CM	950	0	988	56	0
14	AN	492	0	529	27	0
14	CN	492	0	529	29	0
15	AO	728	0	760	16	0
15	CO	728	0	760	27	0
16	AP	681	0	697	32	0
16	CP	677	0	686	29	0
17	AQ	823	0	891	21	0
17	CQ	823	0	891	18	0
18	AR	555	0	618	19	0
18	CR	555	0	618	30	0
19	AS	652	0	662	37	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	CS	646	0	644	56	0
20	AT	728	0	798	32	0
20	CT	727	0	796	30	0
21	AU	199	0	208	5	0
21	CU	199	0	208	7	0
22	AV	114	0	54	0	0
22	CV	113	0	54	0	0
23	AX	1623	0	823	18	0
23	CX	1623	0	824	24	0
24	AW	93	0	84	9	0
24	CW	93	0	84	14	0
25	BA	58834	0	29667	792	0
25	DA	58458	0	29482	1101	0
26	BB	2573	0	1306	39	0
26	DB	2573	0	1306	54	0
27	BD	2136	0	2218	67	0
27	DD	2136	0	2218	74	0
28	BE	1559	0	1618	41	0
28	DE	1559	0	1618	61	0
29	BF	1584	0	1625	49	0
29	DF	1580	0	1619	71	0
30	BG	1425	0	1443	46	0
30	DG	1424	0	1434	87	0
31	BH	1330	0	1407	34	0
31	DH	1330	0	1407	54	0
32	BI	1085	0	1114	44	0
32	DI	1061	0	1080	31	0
33	BN	1117	0	1183	17	0
33	DN	1117	0	1184	26	0
34	BO	933	0	996	27	0
34	DO	933	0	996	37	0
35	BP	1135	0	1212	38	0
35	DP	1135	0	1211	50	0
36	BQ	1122	0	1179	41	0
36	DQ	1122	0	1179	50	0
37	BR	968	0	1033	25	0
37	DR	968	0	1032	32	0
38	BS	877	0	938	26	0
38	DS	870	0	923	47	0
39	BT	1091	0	1151	31	0
39	DT	1083	0	1136	36	0
40	BU	959	0	1019	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	DU	959	0	1019	35	0
41	BV	771	0	830	11	0
41	DV	771	0	830	23	0
42	BW	886	0	940	9	0
42	DW	886	0	940	17	0
43	BX	750	0	814	19	0
43	DX	750	0	814	25	0
44	BY	806	0	881	25	0
44	DY	806	0	881	22	0
45	BZ	1349	0	1355	45	0
45	DZ	1360	0	1363	50	0
46	B0	653	0	674	25	0
46	D0	653	0	674	22	0
47	B1	755	0	826	19	0
47	D1	755	0	826	27	0
48	B2	588	0	643	17	0
48	D2	588	0	643	20	0
49	B3	469	0	518	18	0
49	D3	464	0	514	13	0
50	B4	551	0	532	45	0
50	D4	531	0	502	34	0
51	B5	455	0	465	14	0
51	D5	455	0	465	12	0
52	B6	453	0	473	10	0
52	D6	449	0	469	10	0
53	B7	418	0	466	8	0
53	D7	418	0	467	9	0
54	B8	511	0	571	28	0
54	D8	517	0	582	26	0
55	B9	307	0	335	5	0
55	D9	307	0	335	11	0
56	AA	221	0	0	0	0
56	AD	1	0	0	0	0
56	AF	1	0	0	0	0
56	AK	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	2	0	0	0	0
56	AV	1	0	0	0	0
56	AX	9	0	0	0	0
56	B0	4	0	0	0	0
56	B1	1	0	0	0	0
56	B2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	B3	3	0	0	0	0
56	B4	1	0	0	0	0
56	B5	1	0	0	0	0
56	B7	4	0	0	0	0
56	B8	3	0	0	0	0
56	B9	1	0	0	0	0
56	BA	738	0	0	0	0
56	BB	18	0	0	0	0
56	BD	12	0	0	0	0
56	BE	10	0	0	0	0
56	BF	8	0	0	0	0
56	BG	4	0	0	0	0
56	BN	6	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	5	0	0	0	0
56	BR	4	0	0	0	0
56	BU	8	0	0	0	0
56	BV	4	0	0	0	0
56	BW	5	0	0	0	0
56	BX	1	0	0	0	0
56	BY	1	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	172	0	0	0	0
56	CE	2	0	0	0	0
56	CF	1	0	0	0	0
56	CQ	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	3	0	0	0	0
56	D0	1	0	0	0	0
56	D3	1	0	0	0	0
56	D5	2	0	0	0	0
56	D8	1	0	0	0	0
56	DA	653	0	0	0	0
56	DB	12	0	0	0	0
56	DD	8	0	0	0	0
56	DE	6	0	0	0	0
56	DF	6	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DO	1	0	0	0	0
56	DQ	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	DR	2	0	0	0	0
56	DV	4	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AD	8	0	0	1	0
57	CD	8	0	0	1	0
58	AN	1	0	0	0	0
58	B4	1	0	0	0	0
58	B5	1	0	0	0	0
58	B6	1	0	0	0	0
58	B9	1	0	0	0	0
58	BY	1	0	0	0	0
58	CN	1	0	0	0	0
58	D4	1	0	0	0	0
58	D5	1	0	0	0	0
58	D6	1	0	0	0	0
58	D9	1	0	0	0	0
58	DY	1	0	0	0	0
59	AX	10	0	10	0	0
59	CX	10	0	10	2	0
60	BA	1	0	0	0	0
60	DA	1	0	0	0	0
61	AA	148	0	0	27	0
61	AD	1	0	0	0	0
61	AE	3	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	1	0	0	0	0
61	AP	1	0	0	0	0
61	AU	1	0	0	0	0
61	AV	1	0	0	0	0
61	AX	1	0	0	0	0
61	B0	4	0	0	0	0
61	B1	2	0	0	0	0
61	B5	3	0	0	1	0
61	B7	1	0	0	1	0
61	B8	8	0	0	1	0
61	BA	1092	0	0	113	0
61	BB	26	0	0	0	0
61	BD	8	0	0	1	0
61	BE	9	0	0	4	0
61	BF	4	0	0	0	0
61	BG	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	BN	3	0	0	0	0
61	BO	2	0	0	0	0
61	BP	15	0	0	3	0
61	BQ	3	0	0	1	0
61	BR	1	0	0	0	0
61	BT	1	0	0	0	0
61	BU	4	0	0	0	0
61	BV	2	0	0	0	0
61	BW	2	0	0	0	0
61	BX	4	0	0	1	0
61	CA	187	0	0	24	0
61	CE	2	0	0	0	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CX	2	0	0	0	0
61	D0	5	0	0	1	0
61	D1	1	0	0	0	0
61	D7	2	0	0	0	0
61	D8	4	0	0	0	0
61	DA	902	0	0	119	0
61	DB	7	0	0	0	0
61	DD	8	0	0	0	0
61	DE	13	0	0	1	0
61	DF	5	0	0	0	0
61	DO	1	0	0	0	0
61	DP	14	0	0	0	0
61	DQ	3	0	0	1	0
61	DU	4	0	0	0	0
61	DV	1	0	0	0	0
61	DX	2	0	0	0	0
61	DY	2	0	0	0	0
All	All	286321	0	191126	6489	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 6489 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1002:G:H1	1:CA:1038:C:N4	1.42	1.16
1:AA:348:G:H2'	1:AA:349:A:H5'	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1125:U:N3	1:AA:1127:G:N7	2.06	1.03
39:BT:16:ARG:NH2	39:BT:83:ILE:O	1.92	1.02
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.40	1.02

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	AB	229/256 (90%)	200 (87%)	23 (10%)	6 (3%)	4 21
2	CB	229/256 (90%)	201 (88%)	18 (8%)	10 (4%)	2 12
3	AC	204/239 (85%)	179 (88%)	22 (11%)	3 (2%)	8 32
3	CC	204/239 (85%)	178 (87%)	24 (12%)	2 (1%)	12 41
4	AD	206/209 (99%)	182 (88%)	22 (11%)	2 (1%)	12 41
4	CD	206/209 (99%)	185 (90%)	18 (9%)	3 (2%)	8 32
5	AE	146/162 (90%)	127 (87%)	15 (10%)	4 (3%)	4 20
5	CE	146/162 (90%)	133 (91%)	10 (7%)	3 (2%)	5 25
6	AF	98/101 (97%)	92 (94%)	6 (6%)	0	100 100
6	CF	98/101 (97%)	93 (95%)	5 (5%)	0	100 100
7	AG	153/156 (98%)	137 (90%)	14 (9%)	2 (1%)	9 35
7	CG	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	18 49
8	AH	135/138 (98%)	129 (96%)	6 (4%)	0	100 100
8	CH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	18 49
9	AI	125/128 (98%)	111 (89%)	10 (8%)	4 (3%)	3 18
9	CI	125/128 (98%)	112 (90%)	11 (9%)	2 (2%)	7 30
10	AJ	95/105 (90%)	85 (90%)	7 (7%)	3 (3%)	3 18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
10	CJ	94/105 (90%)	86 (92%)	7 (7%)	1 (1%)	11 39
11	AK	112/129 (87%)	98 (88%)	13 (12%)	1 (1%)	14 44
11	CK	112/129 (87%)	99 (88%)	12 (11%)	1 (1%)	14 44
12	AL	120/132 (91%)	116 (97%)	4 (3%)	0	100 100
12	CL	120/132 (91%)	112 (93%)	8 (7%)	0	100 100
13	AM	121/126 (96%)	106 (88%)	15 (12%)	0	100 100
13	CM	120/126 (95%)	104 (87%)	14 (12%)	2 (2%)	7 30
14	AN	58/61 (95%)	54 (93%)	4 (7%)	0	100 100
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
15	AO	86/89 (97%)	82 (95%)	4 (5%)	0	100 100
15	CO	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10 37
16	AP	80/88 (91%)	69 (86%)	11 (14%)	0	100 100
16	CP	80/88 (91%)	70 (88%)	10 (12%)	0	100 100
17	AQ	97/105 (92%)	91 (94%)	6 (6%)	0	100 100
17	CQ	97/105 (92%)	93 (96%)	4 (4%)	0	100 100
18	AR	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	8 32
18	CR	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	8 32
19	AS	81/93 (87%)	74 (91%)	7 (9%)	0	100 100
19	CS	81/93 (87%)	69 (85%)	12 (15%)	0	100 100
20	AT	94/106 (89%)	84 (89%)	5 (5%)	5 (5%)	1 10
20	CT	94/106 (89%)	85 (90%)	3 (3%)	6 (6%)	1 6
21	AU	21/27 (78%)	17 (81%)	4 (19%)	0	100 100
21	CU	21/27 (78%)	18 (86%)	1 (5%)	2 (10%)	0 3
24	AW	3/10 (30%)	1 (33%)	0	2 (67%)	0 0
24	CW	3/10 (30%)	1 (33%)	1 (33%)	1 (33%)	0 0
27	BD	273/276 (99%)	259 (95%)	13 (5%)	1 (0%)	30 61
27	DD	273/276 (99%)	257 (94%)	13 (5%)	3 (1%)	11 39
28	BE	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	24 57
28	DE	202/206 (98%)	194 (96%)	6 (3%)	2 (1%)	12 41
29	BF	201/210 (96%)	193 (96%)	7 (4%)	1 (0%)	24 57
29	DF	201/210 (96%)	189 (94%)	10 (5%)	2 (1%)	12 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
30	BG	179/182 (98%)	163 (91%)	13 (7%)	3 (2%)	7 30
30	DG	179/182 (98%)	160 (89%)	13 (7%)	6 (3%)	3 16
31	BH	172/180 (96%)	161 (94%)	10 (6%)	1 (1%)	21 52
31	DH	172/180 (96%)	159 (92%)	11 (6%)	2 (1%)	10 37
32	BI	144/148 (97%)	122 (85%)	17 (12%)	5 (4%)	3 16
32	DI	144/148 (97%)	123 (85%)	17 (12%)	4 (3%)	4 20
33	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100 100
33	DN	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	18 49
34	BO	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	16 47
34	DO	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16 47
35	BP	147/150 (98%)	132 (90%)	14 (10%)	1 (1%)	18 49
35	DP	147/150 (98%)	133 (90%)	12 (8%)	2 (1%)	9 34
36	BQ	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18 49
36	DQ	139/141 (99%)	129 (93%)	8 (6%)	2 (1%)	9 34
37	BR	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	14 44
37	DR	116/118 (98%)	109 (94%)	7 (6%)	0	100 100
38	BS	108/112 (96%)	100 (93%)	7 (6%)	1 (1%)	14 44
38	DS	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	14 44
39	BT	129/146 (88%)	124 (96%)	4 (3%)	1 (1%)	16 47
39	DT	129/146 (88%)	125 (97%)	4 (3%)	0	100 100
40	BU	114/118 (97%)	114 (100%)	0	0	100 100
40	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
41	BV	99/101 (98%)	91 (92%)	7 (7%)	1 (1%)	12 41
41	DV	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	12 41
42	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
42	DW	110/113 (97%)	108 (98%)	2 (2%)	0	100 100
43	BX	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11 39
43	DX	93/96 (97%)	87 (94%)	6 (6%)	0	100 100
44	BY	105/110 (96%)	95 (90%)	10 (10%)	0	100 100
44	DY	105/110 (96%)	97 (92%)	8 (8%)	0	100 100
45	BZ	169/206 (82%)	150 (89%)	17 (10%)	2 (1%)	10 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
45	DZ	172/206 (84%)	157 (91%)	15 (9%)	0	100 100
46	B0	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	10 37
46	D0	81/85 (95%)	76 (94%)	5 (6%)	0	100 100
47	B1	95/98 (97%)	93 (98%)	0	2 (2%)	5 25
47	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11 39
48	B2	68/72 (94%)	66 (97%)	2 (3%)	0	100 100
48	D2	68/72 (94%)	65 (96%)	3 (4%)	0	100 100
49	B3	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
49	D3	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
50	B4	67/71 (94%)	50 (75%)	9 (13%)	8 (12%)	0 1
50	D4	67/71 (94%)	50 (75%)	8 (12%)	9 (13%)	0 1
51	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
51	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
52	B6	51/54 (94%)	48 (94%)	3 (6%)	0	100 100
52	D6	51/54 (94%)	48 (94%)	3 (6%)	0	100 100
53	B7	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
53	D7	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	5 24
54	B8	62/65 (95%)	60 (97%)	2 (3%)	0	100 100
54	D8	62/65 (95%)	59 (95%)	3 (5%)	0	100 100
55	B9	35/37 (95%)	35 (100%)	0	0	100 100
55	D9	35/37 (95%)	35 (100%)	0	0	100 100
All	All	11415/12148 (94%)	10525 (92%)	749 (7%)	141 (1%)	10 37

5 of 141 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	17	PHE
2	AB	125	PRO
3	AC	65	ALA
3	AC	107	GLN
4	AD	166	LYS

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	AB	192/220 (87%)	143 (74%)	49 (26%)	0 2
2	CB	187/220 (85%)	144 (77%)	43 (23%)	1 4
3	AC	143/188 (76%)	121 (85%)	22 (15%)	2 12
3	CC	140/188 (74%)	115 (82%)	25 (18%)	2 9
4	AD	170/181 (94%)	142 (84%)	28 (16%)	2 11
4	CD	173/181 (96%)	146 (84%)	27 (16%)	2 12
5	AE	113/123 (92%)	100 (88%)	13 (12%)	5 23
5	CE	114/123 (93%)	103 (90%)	11 (10%)	8 30
6	AF	83/90 (92%)	74 (89%)	9 (11%)	6 25
6	CF	85/90 (94%)	79 (93%)	6 (7%)	13 41
7	AG	119/127 (94%)	90 (76%)	29 (24%)	1 3
7	CG	120/127 (94%)	97 (81%)	23 (19%)	1 7
8	AH	114/119 (96%)	94 (82%)	20 (18%)	2 9
8	CH	114/119 (96%)	95 (83%)	19 (17%)	2 10
9	AI	90/99 (91%)	74 (82%)	16 (18%)	2 9
9	CI	89/99 (90%)	74 (83%)	15 (17%)	2 10
10	AJ	66/92 (72%)	57 (86%)	9 (14%)	3 16
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	9 34
11	AK	82/99 (83%)	72 (88%)	10 (12%)	5 20
11	CK	83/99 (84%)	74 (89%)	9 (11%)	6 25
12	AL	97/109 (89%)	88 (91%)	9 (9%)	8 31
12	CL	97/109 (89%)	86 (89%)	11 (11%)	5 23
13	AM	93/101 (92%)	81 (87%)	12 (13%)	4 18
13	CM	92/101 (91%)	78 (85%)	14 (15%)	3 13
14	AN	49/50 (98%)	40 (82%)	9 (18%)	1 8
14	CN	49/50 (98%)	42 (86%)	7 (14%)	3 14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	AO	78/80 (98%)	67 (86%)	11 (14%)	3 15
15	CO	78/80 (98%)	65 (83%)	13 (17%)	2 10
16	AP	69/74 (93%)	58 (84%)	11 (16%)	2 12
16	CP	68/74 (92%)	60 (88%)	8 (12%)	5 21
17	AQ	94/97 (97%)	88 (94%)	6 (6%)	16 44
17	CQ	94/97 (97%)	84 (89%)	10 (11%)	6 26
18	AR	59/77 (77%)	54 (92%)	5 (8%)	10 35
18	CR	59/77 (77%)	51 (86%)	8 (14%)	3 16
19	AS	69/80 (86%)	62 (90%)	7 (10%)	7 28
19	CS	67/80 (84%)	54 (81%)	13 (19%)	1 7
20	AT	70/82 (85%)	59 (84%)	11 (16%)	2 12
20	CT	70/82 (85%)	58 (83%)	12 (17%)	2 10
21	AU	18/22 (82%)	14 (78%)	4 (22%)	1 4
21	CU	18/22 (82%)	16 (89%)	2 (11%)	6 24
24	AW	3/3 (100%)	2 (67%)	1 (33%)	0 0
24	CW	3/3 (100%)	2 (67%)	1 (33%)	0 0
27	BD	215/218 (99%)	190 (88%)	25 (12%)	5 22
27	DD	215/218 (99%)	190 (88%)	25 (12%)	5 22
28	BE	164/166 (99%)	138 (84%)	26 (16%)	2 12
28	DE	164/166 (99%)	139 (85%)	25 (15%)	3 13
29	BF	160/166 (96%)	135 (84%)	25 (16%)	2 12
29	DF	159/166 (96%)	140 (88%)	19 (12%)	5 21
30	BG	143/156 (92%)	119 (83%)	24 (17%)	2 10
30	DG	142/156 (91%)	118 (83%)	24 (17%)	2 10
31	BH	144/148 (97%)	128 (89%)	16 (11%)	6 24
31	DH	144/148 (97%)	126 (88%)	18 (12%)	4 19
32	BI	110/124 (89%)	82 (74%)	28 (26%)	0 2
32	DI	104/124 (84%)	85 (82%)	19 (18%)	2 8
33	BN	118/119 (99%)	100 (85%)	18 (15%)	3 12
33	DN	118/119 (99%)	99 (84%)	19 (16%)	2 11
34	BO	100/100 (100%)	91 (91%)	9 (9%)	9 33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
34	DO	100/100 (100%)	85 (85%)	15 (15%)	3 13
35	BP	115/116 (99%)	98 (85%)	17 (15%)	3 13
35	DP	115/116 (99%)	97 (84%)	18 (16%)	2 12
36	BQ	111/111 (100%)	96 (86%)	15 (14%)	4 16
36	DQ	111/111 (100%)	96 (86%)	15 (14%)	4 16
37	BR	101/101 (100%)	82 (81%)	19 (19%)	1 7
37	DR	101/101 (100%)	83 (82%)	18 (18%)	2 9
38	BS	87/88 (99%)	72 (83%)	15 (17%)	2 10
38	DS	85/88 (97%)	65 (76%)	20 (24%)	1 3
39	BT	115/127 (91%)	101 (88%)	14 (12%)	5 20
39	DT	113/127 (89%)	100 (88%)	13 (12%)	5 23
40	BU	93/94 (99%)	82 (88%)	11 (12%)	5 21
40	DU	93/94 (99%)	82 (88%)	11 (12%)	5 21
41	BV	80/82 (98%)	66 (82%)	14 (18%)	2 9
41	DV	80/82 (98%)	65 (81%)	15 (19%)	1 7
42	BW	90/92 (98%)	80 (89%)	10 (11%)	6 24
42	DW	90/92 (98%)	78 (87%)	12 (13%)	4 17
43	BX	77/78 (99%)	71 (92%)	6 (8%)	11 38
43	DX	77/78 (99%)	72 (94%)	5 (6%)	15 44
44	BY	85/91 (93%)	79 (93%)	6 (7%)	13 41
44	DY	85/91 (93%)	80 (94%)	5 (6%)	18 48
45	BZ	145/179 (81%)	118 (81%)	27 (19%)	1 8
45	DZ	145/179 (81%)	127 (88%)	18 (12%)	4 19
46	B0	65/67 (97%)	61 (94%)	4 (6%)	16 46
46	D0	65/67 (97%)	59 (91%)	6 (9%)	8 31
47	B1	80/83 (96%)	70 (88%)	10 (12%)	4 19
47	D1	80/83 (96%)	69 (86%)	11 (14%)	3 15
48	B2	65/67 (97%)	55 (85%)	10 (15%)	2 12
48	D2	65/67 (97%)	57 (88%)	8 (12%)	4 20
49	B3	51/52 (98%)	42 (82%)	9 (18%)	2 9
49	D3	50/52 (96%)	41 (82%)	9 (18%)	2 8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
50	B4	59/63 (94%)	46 (78%)	13 (22%)	1 4
50	D4	53/63 (84%)	43 (81%)	10 (19%)	1 7
51	B5	50/52 (96%)	43 (86%)	7 (14%)	3 15
51	D5	50/52 (96%)	46 (92%)	4 (8%)	11 37
52	B6	51/52 (98%)	45 (88%)	6 (12%)	5 21
52	D6	50/52 (96%)	46 (92%)	4 (8%)	11 37
53	B7	41/42 (98%)	37 (90%)	4 (10%)	7 29
53	D7	41/42 (98%)	36 (88%)	5 (12%)	5 20
54	B8	53/55 (96%)	49 (92%)	4 (8%)	12 39
54	D8	54/55 (98%)	49 (91%)	5 (9%)	8 31
55	B9	34/34 (100%)	31 (91%)	3 (9%)	9 33
55	D9	34/34 (100%)	31 (91%)	3 (9%)	9 33
All	All	9325/10072 (93%)	7977 (86%)	1348 (14%)	3 14

5 of 1348 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	CQ	60	ILE
35	DP	98	GLU
19	CS	71	LEU
17	CQ	53	LEU
30	DG	28	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 154 such sidechains are listed below:

Mol	Chain	Res	Type
19	CS	65	ASN
42	DW	62	HIS
27	DD	112	GLN
32	DI	43	ASN
48	D2	38	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1522 (98%)	395 (26%)	25 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CA	1502/1522 (98%)	389 (25%)	31 (2%)
22	AV	4/24 (16%)	1 (25%)	0
22	CV	4/24 (16%)	1 (25%)	0
23	AX	75/77 (97%)	16 (21%)	0
23	CX	75/77 (97%)	16 (21%)	0
25	BA	2722/2915 (93%)	516 (18%)	40 (1%)
25	DA	2704/2915 (92%)	540 (19%)	37 (1%)
26	BB	119/122 (97%)	18 (15%)	0
26	DB	119/122 (97%)	24 (20%)	1 (0%)
All	All	8819/9320 (94%)	1916 (21%)	134 (1%)

5 of 1916 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	9	G
1	AA	15	G
1	AA	22	G
1	AA	32	A

5 of 134 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	DA	1420	U
25	DA	1558	A
25	DA	2689	U
25	BA	1507	A
25	BA	1466	U

5.4 Non-standard residues in protein, DNA, RNA chains (i)

14 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
24	MVA	CW	9	24	6,7,8	0.98	1 (16%)	6,8,10	1.63	2 (33%)
24	MVA	AW	9	24	6,7,8	0.45	0	6,8,10	1.08	1 (16%)
24	MVA	AW	5	24	6,7,8	0.38	0	6,8,10	0.96	0
24	2R3	AW	8	24	12,14,15	0.82	0	16,18,20	1.74	5 (31%)
24	2R3	CW	8	24	12,14,15	0.68	0	16,18,20	1.65	4 (25%)
24	004	AW	3	24	9,10,11	1.11	1 (11%)	9,12,14	1.54	3 (33%)
24	2QY	CW	10	24	12,13,14	2.05	2 (16%)	14,16,18	3.33	3 (21%)
24	2QZ	CW	1	24	7,8,9	0.63	0	7,10,12	3.86	1 (14%)
24	MVA	CW	5	24	6,7,8	0.70	0	6,8,10	1.55	1 (16%)
24	2QZ	AW	1	24	7,8,9	0.40	0	7,10,12	4.39	1 (14%)
24	2R1	AW	6	24	10,10,11	2.21	3 (30%)	8,13,15	4.70	3 (37%)
24	2R1	CW	6	24	10,10,11	1.94	2 (20%)	8,13,15	3.97	3 (37%)
24	004	CW	3	24	9,10,11	1.34	2 (22%)	9,12,14	1.05	0
24	2QY	AW	10	24	12,13,14	1.82	2 (16%)	14,16,18	3.99	5 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	MVA	CW	9	24	-	5/6/8/10	-
24	MVA	AW	9	24	-	4/6/8/10	-
24	MVA	AW	5	24	-	3/6/8/10	-
24	2R3	AW	8	24	-	4/11/12/14	0/1/1/1
24	2R3	CW	8	24	-	7/11/12/14	0/1/1/1
24	004	AW	3	24	-	0/4/6/8	0/1/1/1
24	2QY	CW	10	24	-	2/5/8/10	0/1/1/1
24	2QZ	CW	1	24	-	1/8/10/12	-
24	MVA	CW	5	24	-	5/6/8/10	-
24	2QZ	AW	1	24	-	3/8/10/12	-
24	2R1	AW	6	24	-	1/2/14/16	0/1/1/1
24	2R1	CW	6	24	-	0/2/14/16	0/1/1/1
24	004	CW	3	24	-	0/4/6/8	0/1/1/1
24	2QY	AW	10	24	-	3/5/8/10	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CW	10	2QY	C-CA	5.98	1.53	1.43
24	AW	10	2QY	C-CA	5.42	1.52	1.43
24	AW	6	2R1	OD1-CG1	4.56	1.55	1.42
24	CW	6	2R1	CA-N	4.04	1.46	1.36
24	AW	6	2R1	CA-N	3.71	1.45	1.36

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	AW	6	2R1	OD2-CG2-CB	-12.41	88.98	111.99
24	AW	1	2QZ	OG1-CB-CG2	11.13	142.97	109.68
24	AW	10	2QY	CN-N-CA	-10.64	107.83	123.98
24	CW	6	2R1	OD2-CG2-CB	-9.99	93.46	111.99
24	CW	10	2QY	CN-N-CA	-9.73	109.22	123.98

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	AW	1	2QZ	N-CA-CB-OG1
24	AW	1	2QZ	C-CA-CB-OG1
24	AW	5	MVA	CB-CA-N-CN
24	AW	5	MVA	C-CA-CB-CG1
24	AW	5	MVA	C-CA-CB-CG2

There are no ring outliers.

13 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	CW	9	MVA	6	0
24	AW	9	MVA	3	0
24	AW	8	2R3	1	0
24	CW	8	2R3	2	0
24	AW	3	004	1	0
24	CW	10	2QY	9	0
24	CW	1	2QZ	2	0
24	CW	5	MVA	2	0
24	AW	1	2QZ	2	0
24	AW	6	2R1	1	0
24	CW	6	2R1	1	0
24	CW	3	004	1	0
24	AW	10	2QY	5	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1991 ligands modelled in this entry, 1987 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
59	FME	CX	101	23	8,9,10	0.99	0	8,9,11	1.45	3 (37%)
59	FME	AX	101	23	8,9,10	0.87	0	8,9,11	1.63	2 (25%)
57	SF4	CD	501	4	0,12,12	-	-	-		
57	SF4	AD	501	4	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	FME	CX	101	23	-	3/7/9/11	-
59	FME	AX	101	23	-	3/7/9/11	-
57	SF4	CD	501	4	-	-	0/6/5/5
57	SF4	AD	501	4	-	-	0/6/5/5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	AX	101	FME	CA-N-CN	-2.85	118.44	122.82
59	AX	101	FME	CB-CA-N	2.41	114.90	110.52
59	CX	101	FME	CA-N-CN	-2.17	119.49	122.82
59	CX	101	FME	CB-CA-N	2.17	114.47	110.52
59	CX	101	FME	C-CA-N	2.08	113.52	109.50

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	AX	101	FME	O1-CN-N-CA
59	AX	101	FME	O-C-CA-CB
59	CX	101	FME	O1-CN-N-CA
59	CX	101	FME	O-C-CA-CB
59	CX	101	FME	CA-CB-CG-SD

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	CX	101	FME	2	0
57	CD	501	SF4	1	0
57	AD	501	SF4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	1498/1522 (98%)	-0.09	21 (1%) 73 53	36, 80, 103, 123	0
1	CA	1503/1522 (98%)	-0.05	20 (1%) 75 56	38, 80, 103, 122	0
2	AB	231/256 (90%)	0.38	8 (3%) 47 27	71, 88, 98, 107	0
2	CB	231/256 (90%)	0.49	4 (1%) 69 48	71, 89, 99, 108	0
3	AC	206/239 (86%)	0.34	5 (2%) 59 38	74, 87, 96, 108	0
3	CC	206/239 (86%)	0.56	7 (3%) 48 28	75, 89, 98, 106	0
4	AD	208/209 (99%)	0.51	6 (2%) 53 32	62, 80, 92, 99	0
4	CD	208/209 (99%)	0.32	3 (1%) 73 53	61, 79, 92, 99	0
5	AE	148/162 (91%)	0.01	2 (1%) 73 53	53, 73, 83, 96	0
5	CE	148/162 (91%)	0.14	1 (0%) 84 68	54, 74, 85, 98	0
6	AF	100/101 (99%)	0.16	0 100 100	60, 78, 89, 92	0
6	CF	100/101 (99%)	0.17	1 (1%) 79 61	62, 79, 89, 94	0
7	AG	155/156 (99%)	0.20	2 (1%) 75 56	74, 85, 97, 104	0
7	CG	155/156 (99%)	0.32	6 (3%) 43 24	76, 86, 99, 105	0
8	AH	137/138 (99%)	0.16	1 (0%) 84 68	60, 75, 83, 90	0
8	CH	137/138 (99%)	0.16	0 100 100	61, 76, 83, 90	0
9	AI	127/128 (99%)	0.77	9 (7%) 22 12	70, 92, 99, 103	0
9	CI	127/128 (99%)	1.27	28 (22%) 2 1	69, 93, 100, 105	0
10	AJ	97/105 (92%)	0.80	6 (6%) 26 14	71, 93, 101, 106	0
10	CJ	96/105 (91%)	1.20	16 (16%) 4 2	75, 95, 102, 107	0
11	AK	114/129 (88%)	-0.08	1 (0%) 81 63	53, 74, 88, 93	0
11	CK	114/129 (88%)	-0.00	0 100 100	54, 76, 88, 93	0
12	AL	122/132 (92%)	0.26	5 (4%) 41 23	56, 68, 80, 86	0
12	CL	122/132 (92%)	0.20	1 (0%) 82 65	55, 68, 79, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AM	123/126 (97%)	0.27	3 (2%) 59 38	67, 83, 95, 104	0
13	CM	122/126 (96%)	0.83	7 (5%) 29 16	77, 91, 101, 105	0
14	AN	60/61 (98%)	0.75	6 (10%) 12 6	74, 85, 95, 97	0
14	CN	60/61 (98%)	1.18	9 (15%) 5 3	77, 88, 95, 100	0
15	AO	88/89 (98%)	0.04	1 (1%) 78 59	59, 73, 87, 94	0
15	CO	88/89 (98%)	0.13	2 (2%) 61 39	58, 73, 87, 95	0
16	AP	82/88 (93%)	0.56	2 (2%) 59 38	66, 77, 88, 95	0
16	CP	82/88 (93%)	0.54	2 (2%) 59 38	66, 76, 88, 93	0
17	AQ	99/105 (94%)	0.26	1 (1%) 79 61	59, 73, 84, 87	0
17	CQ	99/105 (94%)	0.17	1 (1%) 79 61	60, 73, 84, 85	0
18	AR	68/88 (77%)	0.01	0 100 100	66, 76, 86, 90	0
18	CR	68/88 (77%)	0.20	1 (1%) 72 52	67, 77, 87, 89	0
19	AS	83/93 (89%)	0.70	7 (8%) 17 9	79, 91, 100, 105	0
19	CS	83/93 (89%)	1.03	13 (15%) 5 2	82, 92, 102, 106	0
20	AT	96/106 (90%)	0.53	9 (9%) 14 8	62, 75, 88, 91	0
20	CT	96/106 (90%)	0.33	3 (3%) 51 30	62, 75, 86, 94	0
21	AU	23/27 (85%)	1.26	1 (4%) 40 22	76, 87, 90, 91	0
21	CU	23/27 (85%)	1.38	5 (21%) 2 1	77, 87, 91, 92	0
22	AV	7/24 (29%)	0.21	0 100 100	61, 73, 97, 100	0
22	CV	6/24 (25%)	0.17	0 100 100	64, 75, 94, 103	0
23	AX	76/77 (98%)	-0.50	0 100 100	48, 79, 96, 101	0
23	CX	76/77 (98%)	-0.27	0 100 100	47, 81, 98, 101	0
24	AW	3/10 (30%)	0.79	0 100 100	78, 78, 93, 96	0
24	CW	3/10 (30%)	0.68	1 (33%) 1 0	67, 67, 87, 96	0
25	BA	2731/2915 (93%)	-0.68	8 (0%) 90 80	24, 44, 86, 114	0
25	DA	2714/2915 (93%)	-0.69	7 (0%) 90 80	27, 48, 87, 118	0
26	BB	120/122 (98%)	-0.35	0 100 100	41, 68, 81, 96	0
26	DB	120/122 (98%)	0.09	0 100 100	47, 73, 86, 98	0
27	BD	275/276 (99%)	-0.42	0 100 100	24, 41, 62, 85	0
27	DD	275/276 (99%)	-0.34	0 100 100	25, 44, 63, 86	0
28	BE	204/206 (99%)	-0.40	0 100 100	22, 45, 68, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	DE	204/206 (99%)	-0.38	1 (0%) 87 73	24, 47, 70, 90	0
29	BF	203/210 (96%)	-0.11	1 (0%) 87 73	24, 52, 77, 97	0
29	DF	203/210 (96%)	-0.17	0 100 100	25, 56, 79, 96	0
30	BG	181/182 (99%)	0.17	1 (0%) 85 70	61, 76, 89, 100	0
30	DG	181/182 (99%)	0.50	3 (1%) 69 48	65, 79, 91, 100	0
31	BH	174/180 (96%)	0.11	1 (0%) 85 70	49, 67, 81, 85	0
31	DH	174/180 (96%)	0.37	2 (1%) 78 59	54, 72, 85, 89	0
32	BI	146/148 (98%)	0.07	0 100 100	49, 77, 88, 94	0
32	DI	146/148 (98%)	0.12	0 100 100	49, 78, 88, 94	0
33	BN	140/140 (100%)	-0.22	1 (0%) 84 68	33, 48, 71, 78	0
33	DN	140/140 (100%)	-0.19	1 (0%) 84 68	35, 52, 73, 81	0
34	BO	122/122 (100%)	-0.53	0 100 100	23, 40, 61, 76	0
34	DO	122/122 (100%)	-0.37	0 100 100	37, 53, 71, 80	0
35	BP	149/150 (99%)	-0.13	1 (0%) 84 68	25, 54, 77, 83	0
35	DP	149/150 (99%)	-0.06	0 100 100	27, 57, 81, 87	0
36	BQ	141/141 (100%)	-0.07	2 (1%) 73 53	36, 52, 68, 79	0
36	DQ	141/141 (100%)	-0.08	3 (2%) 63 42	38, 55, 71, 81	0
37	BR	118/118 (100%)	-0.54	0 100 100	20, 35, 52, 64	0
37	DR	118/118 (100%)	-0.24	0 100 100	36, 52, 68, 84	0
38	BS	110/112 (98%)	-0.42	0 100 100	35, 54, 71, 85	0
38	DS	110/112 (98%)	0.53	5 (4%) 38 20	65, 81, 92, 95	0
39	BT	131/146 (89%)	-0.36	0 100 100	31, 45, 75, 92	0
39	DT	131/146 (89%)	-0.18	1 (0%) 82 65	45, 59, 80, 90	0
40	BU	116/118 (98%)	-0.67	0 100 100	21, 31, 52, 63	0
40	DU	116/118 (98%)	-0.11	0 100 100	36, 61, 78, 92	0
41	BV	101/101 (100%)	-0.29	0 100 100	27, 53, 73, 80	0
41	DV	101/101 (100%)	-0.26	0 100 100	29, 58, 78, 80	0
42	BW	112/113 (99%)	-0.49	0 100 100	27, 38, 62, 92	0
42	DW	112/113 (99%)	-0.41	0 100 100	30, 42, 64, 94	0
43	BX	95/96 (98%)	-0.15	2 (2%) 63 42	29, 47, 72, 81	0
43	DX	95/96 (98%)	-0.03	1 (1%) 78 59	33, 51, 73, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	BY	107/110 (97%)	0.10	2 (1%) 66 45	39, 61, 80, 89	0
44	DY	107/110 (97%)	0.19	3 (2%) 55 34	43, 65, 82, 92	0
45	BZ	171/206 (83%)	0.12	5 (2%) 53 32	53, 71, 85, 96	0
45	DZ	174/206 (84%)	0.27	1 (0%) 85 70	58, 74, 87, 95	0
46	B0	83/85 (97%)	-0.11	7 (8%) 17 9	25, 39, 80, 108	0
46	D0	83/85 (97%)	0.39	7 (8%) 17 9	42, 66, 86, 104	0
47	B1	97/98 (98%)	-0.37	1 (1%) 79 61	27, 44, 74, 83	0
47	D1	97/98 (98%)	-0.09	1 (1%) 79 61	35, 58, 79, 86	0
48	B2	70/72 (97%)	-0.26	1 (1%) 73 53	35, 48, 64, 90	0
48	D2	70/72 (97%)	0.02	0 100 100	59, 74, 83, 92	0
49	B3	59/60 (98%)	-0.46	0 100 100	24, 38, 63, 85	0
49	D3	59/60 (98%)	-0.19	0 100 100	45, 62, 80, 90	0
50	B4	69/71 (97%)	0.19	0 100 100	60, 85, 103, 105	0
50	D4	69/71 (97%)	0.70	4 (5%) 29 16	82, 96, 106, 112	0
51	B5	59/60 (98%)	-0.68	0 100 100	14, 36, 59, 74	0
51	D5	59/60 (98%)	-0.36	0 100 100	31, 50, 72, 82	0
52	B6	53/54 (98%)	-0.45	0 100 100	43, 53, 68, 75	0
52	D6	53/54 (98%)	-0.15	0 100 100	45, 56, 69, 73	0
53	B7	48/49 (97%)	-0.33	0 100 100	24, 32, 62, 84	0
53	D7	48/49 (97%)	-0.24	1 (2%) 63 42	26, 35, 63, 86	0
54	B8	64/65 (98%)	-0.28	0 100 100	31, 42, 51, 64	0
54	D8	64/65 (98%)	-0.15	0 100 100	34, 46, 56, 66	0
55	B9	37/37 (100%)	0.01	1 (2%) 56 35	43, 53, 71, 77	0
55	D9	37/37 (100%)	0.31	1 (2%) 56 35	46, 58, 73, 78	0
All	All	20462/21468 (95%)	-0.14	303 (1%) 72 52	14, 65, 95, 123	0

The worst 5 of 303 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	7.2
13	CM	123	ALA	6.1
14	CN	2	ALA	5.8
13	AM	123	ALA	5.7
9	CI	105	ASP	5.7

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
24	2R1	AW	6	10/11	0.73	0.14	68,82,98,104	0
24	004	AW	3	10/11	0.76	0.17	71,89,99,106	0
24	2R1	CW	6	10/11	0.76	0.12	79,86,90,94	0
24	MVA	AW	5	8/9	0.81	0.15	66,87,90,90	0
24	2QY	CW	10	13/14	0.87	0.11	55,69,84,94	0
24	2R3	AW	8	14/15	0.89	0.09	54,79,87,90	0
24	004	CW	3	10/11	0.90	0.10	60,76,84,86	0
24	MVA	CW	5	8/9	0.90	0.08	51,78,86,88	0
24	MVA	CW	9	8/9	0.91	0.14	61,72,80,84	0
24	MVA	AW	9	8/9	0.91	0.14	65,78,87,91	0
24	2R3	CW	8	14/15	0.93	0.07	47,70,74,79	0
24	2QZ	CW	1	9/10	0.94	0.12	57,72,81,93	0
24	2QY	AW	10	13/14	0.95	0.06	55,67,75,79	0
24	2QZ	AW	1	9/10	0.95	0.10	58,64,81,82	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BZ	3001	1/1	0.47	0.26	61,61,61,61	0
56	MG	B4	3001	1/1	0.48	0.21	100,100,100,100	0
56	MG	DB	3001	1/1	0.48	0.17	68,68,68,68	0
56	MG	CA	3114	1/1	0.51	0.19	82,82,82,82	0
56	MG	CA	3025	1/1	0.51	0.26	94,94,94,94	0
56	MG	CA	3139	1/1	0.53	0.21	75,75,75,75	0
56	MG	CA	3042	1/1	0.56	0.35	85,85,85,85	0
56	MG	BA	3579	1/1	0.59	0.23	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3093	1/1	0.60	0.38	88,88,88,88	0
56	MG	BA	3247	1/1	0.60	0.17	68,68,68,68	0
56	MG	AA	3147	1/1	0.61	0.17	61,61,61,61	0
56	MG	AA	3087	1/1	0.61	0.18	72,72,72,72	0
56	MG	AA	3061	1/1	0.63	0.13	82,82,82,82	0
56	MG	BA	3353	1/1	0.63	0.14	57,57,57,57	0
56	MG	CA	3110	1/1	0.64	0.22	97,97,97,97	0
56	MG	BA	3140	1/1	0.64	0.23	64,64,64,64	0
56	MG	AA	3132	1/1	0.65	0.32	76,76,76,76	0
56	MG	AA	3120	1/1	0.65	0.35	71,71,71,71	0
56	MG	AA	3164	1/1	0.65	0.20	69,69,69,69	0
56	MG	AA	3084	1/1	0.66	0.41	78,78,78,78	0
56	MG	CA	3147	1/1	0.66	0.17	66,66,66,66	0
56	MG	CA	3127	1/1	0.66	0.22	79,79,79,79	0
56	MG	DA	3464	1/1	0.67	0.21	50,50,50,50	0
56	MG	AA	3129	1/1	0.67	0.26	77,77,77,77	0
56	MG	BA	3622	1/1	0.68	0.23	77,77,77,77	0
56	MG	AA	3067	1/1	0.68	0.34	87,87,87,87	0
56	MG	CA	3030	1/1	0.69	0.32	73,73,73,73	0
56	MG	CA	3067	1/1	0.70	0.25	80,80,80,80	0
56	MG	CA	3081	1/1	0.70	0.16	72,72,72,72	0
56	MG	CA	3109	1/1	0.70	0.16	83,83,83,83	0
56	MG	BA	3658	1/1	0.70	0.18	79,79,79,79	0
56	MG	AA	3030	1/1	0.70	0.41	69,69,69,69	0
56	MG	CA	3038	1/1	0.71	0.19	70,70,70,70	0
56	MG	AA	3013	1/1	0.71	0.11	78,78,78,78	0
56	MG	DA	3615	1/1	0.71	0.16	60,60,60,60	0
56	MG	DA	3638	1/1	0.71	0.20	62,62,62,62	0
56	MG	BA	3088	1/1	0.71	0.14	56,56,56,56	0
56	MG	CA	3070	1/1	0.72	0.16	55,55,55,55	0
56	MG	BA	3023	1/1	0.72	0.21	66,66,66,66	0
56	MG	DA	3062	1/1	0.73	0.15	55,55,55,55	0
56	MG	DA	3256	1/1	0.73	0.16	63,63,63,63	0
56	MG	DA	3553	1/1	0.74	0.15	70,70,70,70	0
56	MG	DA	3598	1/1	0.74	0.13	66,66,66,66	0
56	MG	BA	3462	1/1	0.74	0.14	52,52,52,52	0
56	MG	DA	3635	1/1	0.74	0.20	58,58,58,58	0
56	MG	DA	3284	1/1	0.74	0.12	68,68,68,68	0
56	MG	AA	3022	1/1	0.74	0.17	48,48,48,48	0
56	MG	BA	3288	1/1	0.75	0.26	61,61,61,61	0
56	MG	AA	3136	1/1	0.75	0.16	62,62,62,62	0
56	MG	DA	3410	1/1	0.75	0.28	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3438	1/1	0.75	0.20	70,70,70,70	0
56	MG	AA	3180	1/1	0.75	0.21	66,66,66,66	0
56	MG	DA	3482	1/1	0.75	0.14	55,55,55,55	0
56	MG	DA	3503	1/1	0.75	0.19	71,71,71,71	0
56	MG	CA	3125	1/1	0.75	0.13	72,72,72,72	0
56	MG	CA	3053	1/1	0.75	0.44	73,73,73,73	0
56	MG	BA	3495	1/1	0.75	0.16	84,84,84,84	0
56	MG	CA	3003	1/1	0.75	0.14	66,66,66,66	0
56	MG	CQ	201	1/1	0.75	0.14	56,56,56,56	0
56	MG	AA	3044	1/1	0.75	0.16	66,66,66,66	0
56	MG	DQ	205	1/1	0.75	0.16	55,55,55,55	0
56	MG	BA	3354	1/1	0.76	0.13	74,74,74,74	0
56	MG	BA	3370	1/1	0.76	0.10	54,54,54,54	0
56	MG	DA	3484	1/1	0.76	0.12	51,51,51,51	0
56	MG	DA	3162	1/1	0.76	0.29	71,71,71,71	0
56	MG	DA	3526	1/1	0.76	0.12	54,54,54,54	0
56	MG	DA	3240	1/1	0.76	0.14	51,51,51,51	0
56	MG	BA	3180	1/1	0.76	0.45	43,43,43,43	0
56	MG	BA	3297	1/1	0.76	0.36	53,53,53,53	0
56	MG	BA	3040	1/1	0.76	0.26	51,51,51,51	0
56	MG	DA	3427	1/1	0.76	0.19	60,60,60,60	0
56	MG	CA	3161	1/1	0.76	0.11	54,54,54,54	0
56	MG	DA	3460	1/1	0.76	0.12	50,50,50,50	0
59	FME	CX	101	10/11	0.76	0.32	71,82,97,105	0
56	MG	DA	3492	1/1	0.77	0.16	68,68,68,68	0
56	MG	BA	3089	1/1	0.77	0.12	61,61,61,61	0
56	MG	CA	3135	1/1	0.77	0.27	76,76,76,76	0
56	MG	AA	3131	1/1	0.77	0.24	56,56,56,56	0
56	MG	BA	3669	1/1	0.77	0.17	75,75,75,75	0
56	MG	CA	3153	1/1	0.77	0.15	83,83,83,83	0
56	MG	DA	3623	1/1	0.77	0.15	53,53,53,53	0
56	MG	BN	3002	1/1	0.77	0.11	56,56,56,56	0
56	MG	AA	3162	1/1	0.77	0.21	74,74,74,74	0
56	MG	DA	3001	1/1	0.77	0.30	78,78,78,78	0
56	MG	DB	3011	1/1	0.77	0.19	55,55,55,55	0
56	MG	CA	3047	1/1	0.77	0.17	63,63,63,63	0
56	MG	AA	3218	1/1	0.77	0.33	65,65,65,65	0
56	MG	BB	3014	1/1	0.78	0.19	69,69,69,69	0
56	MG	BA	3157	1/1	0.78	0.18	63,63,63,63	0
56	MG	CE	3001	1/1	0.78	0.31	68,68,68,68	0
56	MG	DA	3624	1/1	0.78	0.22	51,51,51,51	0
56	MG	CA	3048	1/1	0.78	0.27	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3401	1/1	0.78	0.24	58,58,58,58	0
56	MG	AA	3085	1/1	0.78	0.23	69,69,69,69	0
56	MG	BA	3215	1/1	0.78	0.20	69,69,69,69	0
56	MG	DA	3093	1/1	0.78	0.10	53,53,53,53	0
56	MG	DA	3563	1/1	0.78	0.14	64,64,64,64	0
56	MG	DA	3185	1/1	0.79	0.19	52,52,52,52	0
56	MG	DA	3500	1/1	0.79	0.12	50,50,50,50	0
56	MG	DA	3195	1/1	0.79	0.20	50,50,50,50	0
56	MG	DA	3228	1/1	0.79	0.10	45,45,45,45	0
56	MG	BA	3693	1/1	0.79	0.15	64,64,64,64	0
56	MG	BA	3727	1/1	0.79	0.25	68,68,68,68	0
56	MG	DA	3279	1/1	0.79	0.18	63,63,63,63	0
56	MG	DA	3613	1/1	0.79	0.10	54,54,54,54	0
56	MG	CA	3073	1/1	0.79	0.21	55,55,55,55	0
56	MG	CA	3035	1/1	0.79	0.19	52,52,52,52	0
56	MG	BA	3331	1/1	0.79	0.18	47,47,47,47	0
56	MG	CA	3041	1/1	0.79	0.29	75,75,75,75	0
56	MG	BA	3136	1/1	0.79	0.15	58,58,58,58	0
56	MG	BA	3067	1/1	0.79	0.19	53,53,53,53	0
56	MG	DB	3010	1/1	0.79	0.20	73,73,73,73	0
56	MG	AA	3021	1/1	0.79	0.14	76,76,76,76	0
56	MG	DF	302	1/1	0.79	0.09	43,43,43,43	0
56	MG	DA	3099	1/1	0.79	0.17	44,44,44,44	0
56	MG	AA	3109	1/1	0.79	0.19	65,65,65,65	0
60	K	DA	3231	1/1	0.79	0.25	96,96,96,96	0
56	MG	AA	3206	1/1	0.80	0.12	70,70,70,70	0
56	MG	AA	3007	1/1	0.80	0.23	82,82,82,82	0
56	MG	DA	3134	1/1	0.80	0.13	46,46,46,46	0
56	MG	AA	3009	1/1	0.80	0.23	79,79,79,79	0
56	MG	CA	3086	1/1	0.80	0.26	80,80,80,80	0
56	MG	BA	3158	1/1	0.80	0.37	64,64,64,64	0
56	MG	BA	3168	1/1	0.80	0.18	42,42,42,42	0
56	MG	CA	3007	1/1	0.80	0.14	68,68,68,68	0
56	MG	AA	3039	1/1	0.80	0.15	60,60,60,60	0
56	MG	BA	3193	1/1	0.80	0.18	52,52,52,52	0
56	MG	CA	3032	1/1	0.80	0.17	42,42,42,42	0
56	MG	DA	3361	1/1	0.80	0.12	61,61,61,61	0
56	MG	BA	3611	1/1	0.80	0.13	52,52,52,52	0
56	MG	AA	3090	1/1	0.80	0.17	68,68,68,68	0
56	MG	BA	3234	1/1	0.80	0.18	55,55,55,55	0
56	MG	AA	3071	1/1	0.80	0.27	60,60,60,60	0
56	MG	BA	3683	1/1	0.80	0.22	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3200	1/1	0.80	0.21	68,68,68,68	0
56	MG	BA	3094	1/1	0.80	0.31	61,61,61,61	0
56	MG	BB	3005	1/1	0.80	0.23	61,61,61,61	0
56	MG	AA	3059	1/1	0.81	0.27	54,54,54,54	0
56	MG	BA	3027	1/1	0.81	0.12	45,45,45,45	0
56	MG	BA	3496	1/1	0.81	0.26	57,57,57,57	0
56	MG	DA	3510	1/1	0.81	0.15	63,63,63,63	0
56	MG	DA	3515	1/1	0.81	0.12	48,48,48,48	0
56	MG	BQ	203	1/1	0.81	0.14	58,58,58,58	0
56	MG	AA	3019	1/1	0.81	0.10	74,74,74,74	0
56	MG	CA	3057	1/1	0.81	0.19	49,49,49,49	0
56	MG	AA	3088	1/1	0.81	0.42	63,63,63,63	0
56	MG	DA	3609	1/1	0.81	0.24	64,64,64,64	0
56	MG	BA	3289	1/1	0.81	0.28	60,60,60,60	0
56	MG	DA	3303	1/1	0.81	0.09	47,47,47,47	0
56	MG	DA	3314	1/1	0.81	0.18	64,64,64,64	0
56	MG	AA	3128	1/1	0.81	0.18	68,68,68,68	0
56	MG	AA	3212	1/1	0.81	0.10	79,79,79,79	0
56	MG	DA	3061	1/1	0.81	0.24	52,52,52,52	0
56	MG	BA	3183	1/1	0.81	0.25	48,48,48,48	0
56	MG	BA	3189	1/1	0.81	0.12	54,54,54,54	0
56	MG	BA	3712	1/1	0.81	0.16	58,58,58,58	0
56	MG	DA	3117	1/1	0.81	0.10	53,53,53,53	0
56	MG	DA	3465	1/1	0.81	0.11	49,49,49,49	0
56	MG	DA	3122	1/1	0.81	0.19	62,62,62,62	0
56	MG	AA	3065	1/1	0.81	0.23	60,60,60,60	0
56	MG	DA	3267	1/1	0.82	0.14	61,61,61,61	0
56	MG	DA	3030	1/1	0.82	0.17	51,51,51,51	0
56	MG	BA	3144	1/1	0.82	0.28	74,74,74,74	0
56	MG	AA	3112	1/1	0.82	0.23	51,51,51,51	0
56	MG	DA	3084	1/1	0.82	0.16	70,70,70,70	0
56	MG	AA	3113	1/1	0.82	0.21	68,68,68,68	0
56	MG	BA	3507	1/1	0.82	0.24	68,68,68,68	0
56	MG	DA	3115	1/1	0.82	0.12	63,63,63,63	0
56	MG	CA	3146	1/1	0.82	0.14	69,69,69,69	0
56	MG	DA	3621	1/1	0.82	0.09	54,54,54,54	0
56	MG	AA	3046	1/1	0.82	0.24	73,73,73,73	0
56	MG	DA	3456	1/1	0.82	0.16	47,47,47,47	0
56	MG	AA	3060	1/1	0.82	0.36	60,60,60,60	0
56	MG	DA	3161	1/1	0.82	0.16	60,60,60,60	0
56	MG	CA	3157	1/1	0.82	0.13	54,54,54,54	0
56	MG	DA	3481	1/1	0.82	0.09	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3094	1/1	0.82	0.11	68,68,68,68	0
56	MG	CA	3170	1/1	0.82	0.22	50,50,50,50	0
56	MG	BA	3099	1/1	0.82	0.19	44,44,44,44	0
56	MG	AA	3089	1/1	0.82	0.31	78,78,78,78	0
56	MG	BA	3029	1/1	0.82	0.34	53,53,53,53	0
56	MG	AX	106	1/1	0.83	0.10	73,73,73,73	0
56	MG	DA	3207	1/1	0.83	0.14	58,58,58,58	0
56	MG	BA	3718	1/1	0.83	0.13	57,57,57,57	0
56	MG	DA	3238	1/1	0.83	0.07	61,61,61,61	0
56	MG	DA	3511	1/1	0.83	0.16	65,65,65,65	0
56	MG	AA	3117	1/1	0.83	0.11	71,71,71,71	0
56	MG	DA	3054	1/1	0.83	0.20	51,51,51,51	0
56	MG	DA	3060	1/1	0.83	0.15	55,55,55,55	0
56	MG	AA	3072	1/1	0.83	0.24	79,79,79,79	0
56	MG	DA	3581	1/1	0.83	0.30	73,73,73,73	0
56	MG	DA	3590	1/1	0.83	0.19	80,80,80,80	0
56	MG	BA	3598	1/1	0.83	0.12	56,56,56,56	0
56	MG	BA	3103	1/1	0.83	0.16	53,53,53,53	0
56	MG	CA	3044	1/1	0.83	0.18	63,63,63,63	0
56	MG	BA	3613	1/1	0.83	0.17	76,76,76,76	0
56	MG	DA	3620	1/1	0.83	0.11	71,71,71,71	0
56	MG	DA	3112	1/1	0.83	0.28	54,54,54,54	0
56	MG	DA	3402	1/1	0.83	0.13	61,61,61,61	0
56	MG	AA	3024	1/1	0.83	0.12	53,53,53,53	0
56	MG	B2	101	1/1	0.83	0.15	40,40,40,40	0
56	MG	AA	3209	1/1	0.83	0.14	70,70,70,70	0
56	MG	DA	3123	1/1	0.83	0.26	59,59,59,59	0
56	MG	DA	3124	1/1	0.83	0.13	67,67,67,67	0
56	MG	DA	3131	1/1	0.83	0.09	54,54,54,54	0
56	MG	AA	3023	1/1	0.83	0.26	65,65,65,65	0
56	MG	DG	3001	1/1	0.83	0.13	63,63,63,63	0
56	MG	BA	3156	1/1	0.83	0.33	56,56,56,56	0
56	MG	DW	202	1/1	0.83	0.15	58,58,58,58	0
59	FME	AX	101	10/11	0.83	0.22	48,75,97,113	0
56	MG	CA	3021	1/1	0.83	0.18	53,53,53,53	0
56	MG	AA	3035	1/1	0.83	0.15	71,71,71,71	0
56	MG	AA	3017	1/1	0.84	0.24	55,55,55,55	0
56	MG	DA	3224	1/1	0.84	0.17	47,47,47,47	0
56	MG	BA	3562	1/1	0.84	0.14	73,73,73,73	0
56	MG	DA	3023	1/1	0.84	0.19	52,52,52,52	0
56	MG	AA	3076	1/1	0.84	0.24	66,66,66,66	0
56	MG	DA	3545	1/1	0.84	0.17	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3580	1/1	0.84	0.15	58,58,58,58	0
56	MG	DA	3557	1/1	0.84	0.16	45,45,45,45	0
56	MG	BW	205	1/1	0.84	0.22	41,41,41,41	0
56	MG	DA	3564	1/1	0.84	0.17	61,61,61,61	0
56	MG	BA	3263	1/1	0.84	0.28	79,79,79,79	0
56	MG	AA	3045	1/1	0.84	0.30	61,61,61,61	0
56	MG	DA	3286	1/1	0.84	0.14	62,62,62,62	0
56	MG	DA	3071	1/1	0.84	0.22	46,46,46,46	0
56	MG	AA	3006	1/1	0.84	0.12	78,78,78,78	0
56	MG	DA	3340	1/1	0.84	0.07	47,47,47,47	0
56	MG	AA	3047	1/1	0.84	0.16	61,61,61,61	0
56	MG	BA	3645	1/1	0.84	0.12	56,56,56,56	0
56	MG	DA	3107	1/1	0.84	0.09	55,55,55,55	0
56	MG	BA	3160	1/1	0.84	0.28	53,53,53,53	0
56	MG	DA	3631	1/1	0.84	0.09	56,56,56,56	0
56	MG	AX	103	1/1	0.84	0.15	66,66,66,66	0
56	MG	AA	3068	1/1	0.84	0.15	66,66,66,66	0
56	MG	AA	3069	1/1	0.84	0.10	84,84,84,84	0
56	MG	CA	3141	1/1	0.84	0.28	70,70,70,70	0
56	MG	BA	3700	1/1	0.84	0.11	67,67,67,67	0
56	MG	BA	3706	1/1	0.84	0.28	63,63,63,63	0
56	MG	BA	3123	1/1	0.84	0.22	69,69,69,69	0
56	MG	BA	3135	1/1	0.84	0.18	42,42,42,42	0
56	MG	AA	3002	1/1	0.84	0.09	57,57,57,57	0
56	MG	BA	3739	1/1	0.84	0.20	50,50,50,50	0
56	MG	DA	3499	1/1	0.84	0.12	46,46,46,46	0
56	MG	BB	3003	1/1	0.84	0.14	43,43,43,43	0
56	MG	CA	3159	1/1	0.85	0.33	91,91,91,91	0
56	MG	DA	3164	1/1	0.85	0.15	48,48,48,48	0
56	MG	DA	3169	1/1	0.85	0.24	57,57,57,57	0
56	MG	DA	3170	1/1	0.85	0.18	57,57,57,57	0
56	MG	BA	3632	1/1	0.85	0.17	57,57,57,57	0
56	MG	CA	3065	1/1	0.85	0.15	75,75,75,75	0
56	MG	BA	3372	1/1	0.85	0.14	38,38,38,38	0
56	MG	BA	3402	1/1	0.85	0.16	71,71,71,71	0
56	MG	DA	3527	1/1	0.85	0.10	46,46,46,46	0
56	MG	DA	3537	1/1	0.85	0.14	65,65,65,65	0
56	MG	CX	103	1/1	0.85	0.15	60,60,60,60	0
56	MG	CA	3071	1/1	0.85	0.15	63,63,63,63	0
56	MG	BA	3405	1/1	0.85	0.10	34,34,34,34	0
56	MG	DA	3248	1/1	0.85	0.22	51,51,51,51	0
56	MG	DA	3252	1/1	0.85	0.15	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AN	103	1/1	0.85	0.19	60,60,60,60	0
56	MG	DA	3039	1/1	0.85	0.23	59,59,59,59	0
56	MG	AA	3195	1/1	0.85	0.24	71,71,71,71	0
56	MG	BA	3276	1/1	0.85	0.19	40,40,40,40	0
56	MG	AA	3102	1/1	0.85	0.19	64,64,64,64	0
56	MG	BA	3061	1/1	0.85	0.28	51,51,51,51	0
56	MG	BA	3065	1/1	0.85	0.11	50,50,50,50	0
56	MG	DA	3074	1/1	0.85	0.18	54,54,54,54	0
56	MG	DA	3357	1/1	0.85	0.12	56,56,56,56	0
56	MG	BA	3205	1/1	0.85	0.10	40,40,40,40	0
56	MG	BA	3334	1/1	0.85	0.25	73,73,73,73	0
56	MG	CA	3138	1/1	0.85	0.18	72,72,72,72	0
56	MG	AA	3189	1/1	0.85	0.11	77,77,77,77	0
56	MG	DA	3654	1/1	0.85	0.27	52,52,52,52	0
56	MG	BA	3221	1/1	0.85	0.19	44,44,44,44	0
56	MG	CA	3142	1/1	0.85	0.08	59,59,59,59	0
56	MG	BB	3009	1/1	0.85	0.13	48,48,48,48	0
56	MG	BA	3617	1/1	0.85	0.18	62,62,62,62	0
56	MG	CA	3148	1/1	0.85	0.16	68,68,68,68	0
56	MG	CA	3150	1/1	0.85	0.08	59,59,59,59	0
56	MG	DA	3479	1/1	0.85	0.20	57,57,57,57	0
56	MG	BA	3075	1/1	0.85	0.09	45,45,45,45	0
56	MG	BA	3628	1/1	0.85	0.21	41,41,41,41	0
60	K	BA	3300	1/1	0.85	0.21	100,100,100,100	0
56	MG	CA	3158	1/1	0.85	0.14	76,76,76,76	0
56	MG	DA	3154	1/1	0.86	0.36	45,45,45,45	0
56	MG	BA	3543	1/1	0.86	0.17	52,52,52,52	0
56	MG	AX	104	1/1	0.86	0.26	76,76,76,76	0
56	MG	BA	3309	1/1	0.86	0.13	46,46,46,46	0
56	MG	CA	3164	1/1	0.86	0.17	49,49,49,49	0
56	MG	DA	3502	1/1	0.86	0.06	65,65,65,65	0
56	MG	CA	3061	1/1	0.86	0.20	46,46,46,46	0
56	MG	CA	3171	1/1	0.86	0.16	67,67,67,67	0
56	MG	BA	3198	1/1	0.86	0.16	52,52,52,52	0
56	MG	BA	3593	1/1	0.86	0.08	74,74,74,74	0
56	MG	DA	3212	1/1	0.86	0.10	48,48,48,48	0
56	MG	CT	3001	1/1	0.86	0.27	57,57,57,57	0
56	MG	AA	3138	1/1	0.86	0.23	37,37,37,37	0
56	MG	AA	3096	1/1	0.86	0.17	44,44,44,44	0
56	MG	DA	3013	1/1	0.86	0.18	47,47,47,47	0
56	MG	AA	3029	1/1	0.86	0.24	52,52,52,52	0
56	MG	AA	3133	1/1	0.86	0.33	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3618	1/1	0.86	0.10	46,46,46,46	0
56	MG	DA	3565	1/1	0.86	0.10	57,57,57,57	0
56	MG	DA	3265	1/1	0.86	0.15	51,51,51,51	0
56	MG	B0	103	1/1	0.86	0.29	59,59,59,59	0
56	MG	AA	3170	1/1	0.86	0.28	101,101,101,101	0
56	MG	BA	3119	1/1	0.86	0.19	58,58,58,58	0
56	MG	AA	3134	1/1	0.86	0.32	70,70,70,70	0
56	MG	BA	3426	1/1	0.86	0.24	51,51,51,51	0
56	MG	BA	3430	1/1	0.86	0.29	49,49,49,49	0
56	MG	DA	3322	1/1	0.86	0.15	55,55,55,55	0
56	MG	DA	3080	1/1	0.86	0.15	44,44,44,44	0
56	MG	CA	3022	1/1	0.86	0.09	70,70,70,70	0
56	MG	BA	3444	1/1	0.86	0.08	74,74,74,74	0
56	MG	DA	3632	1/1	0.86	0.12	71,71,71,71	0
56	MG	BA	3673	1/1	0.86	0.09	53,53,53,53	0
56	MG	BA	3282	1/1	0.86	0.21	49,49,49,49	0
56	MG	DA	3647	1/1	0.86	0.24	66,66,66,66	0
56	MG	BA	3482	1/1	0.86	0.12	72,72,72,72	0
56	MG	DA	3415	1/1	0.86	0.12	56,56,56,56	0
56	MG	AA	3095	1/1	0.86	0.31	58,58,58,58	0
56	MG	AA	3194	1/1	0.86	0.16	54,54,54,54	0
56	MG	DA	3454	1/1	0.86	0.10	55,55,55,55	0
56	MG	CA	3149	1/1	0.86	0.11	74,74,74,74	0
56	MG	DA	3458	1/1	0.86	0.13	71,71,71,71	0
56	MG	BA	3293	1/1	0.86	0.09	45,45,45,45	0
56	MG	BA	3714	1/1	0.86	0.11	58,58,58,58	0
56	MG	CA	3156	1/1	0.86	0.15	70,70,70,70	0
56	MG	BA	3511	1/1	0.86	0.09	39,39,39,39	0
56	MG	DA	3135	1/1	0.86	0.15	50,50,50,50	0
56	MG	DA	3018	1/1	0.87	0.18	48,48,48,48	0
56	MG	BA	3147	1/1	0.87	0.21	46,46,46,46	0
56	MG	DA	3222	1/1	0.87	0.18	71,71,71,71	0
56	MG	DA	3223	1/1	0.87	0.30	66,66,66,66	0
56	MG	DA	3024	1/1	0.87	0.20	65,65,65,65	0
56	MG	CA	3014	1/1	0.87	0.28	50,50,50,50	0
56	MG	AA	3083	1/1	0.87	0.12	65,65,65,65	0
56	MG	DA	3041	1/1	0.87	0.28	57,57,57,57	0
56	MG	DA	3243	1/1	0.87	0.16	67,67,67,67	0
56	MG	CA	3119	1/1	0.87	0.15	64,64,64,64	0
56	MG	AA	3110	1/1	0.87	0.14	48,48,48,48	0
56	MG	AA	3155	1/1	0.87	0.18	70,70,70,70	0
56	MG	AA	3063	1/1	0.87	0.32	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3554	1/1	0.87	0.27	70,70,70,70	0
56	MG	AA	3037	1/1	0.87	0.19	61,61,61,61	0
56	MG	CA	3034	1/1	0.87	0.20	65,65,65,65	0
56	MG	BA	3440	1/1	0.87	0.16	38,38,38,38	0
56	MG	BA	3735	1/1	0.87	0.11	45,45,45,45	0
56	MG	DA	3293	1/1	0.87	0.13	53,53,53,53	0
56	MG	AA	3114	1/1	0.87	0.30	66,66,66,66	0
56	MG	DA	3591	1/1	0.87	0.14	58,58,58,58	0
56	MG	DA	3592	1/1	0.87	0.18	65,65,65,65	0
56	MG	DA	3096	1/1	0.87	0.11	60,60,60,60	0
56	MG	BA	3619	1/1	0.87	0.21	40,40,40,40	0
56	MG	BA	3134	1/1	0.87	0.21	47,47,47,47	0
56	MG	DA	3352	1/1	0.87	0.13	47,47,47,47	0
56	MG	AA	3178	1/1	0.87	0.19	65,65,65,65	0
56	MG	AA	3100	1/1	0.87	0.18	40,40,40,40	0
56	MG	DA	3363	1/1	0.87	0.17	57,57,57,57	0
56	MG	CA	3049	1/1	0.87	0.29	53,53,53,53	0
56	MG	DA	3626	1/1	0.87	0.07	68,68,68,68	0
56	MG	BF	308	1/1	0.87	0.10	28,28,28,28	0
56	MG	CA	3054	1/1	0.87	0.20	48,48,48,48	0
56	MG	BG	3004	1/1	0.87	0.14	62,62,62,62	0
56	MG	BA	3644	1/1	0.87	0.09	43,43,43,43	0
56	MG	DA	3640	1/1	0.87	0.41	56,56,56,56	0
56	MG	CA	3063	1/1	0.87	0.12	61,61,61,61	0
56	MG	AA	3079	1/1	0.87	0.39	74,74,74,74	0
56	MG	AA	3190	1/1	0.87	0.21	67,67,67,67	0
56	MG	BA	3661	1/1	0.87	0.10	68,68,68,68	0
56	MG	BA	3664	1/1	0.87	0.21	68,68,68,68	0
56	MG	BA	3206	1/1	0.87	0.15	57,57,57,57	0
56	MG	BA	3146	1/1	0.87	0.15	52,52,52,52	0
56	MG	BA	3216	1/1	0.87	0.17	41,41,41,41	0
56	MG	CA	3103	1/1	0.87	0.16	83,83,83,83	0
56	MG	D0	101	1/1	0.87	0.12	63,63,63,63	0
56	MG	D5	101	1/1	0.87	0.33	53,53,53,53	0
56	MG	DA	3186	1/1	0.87	0.14	53,53,53,53	0
56	MG	CA	3105	1/1	0.87	0.10	79,79,79,79	0
56	MG	DA	3487	1/1	0.87	0.17	57,57,57,57	0
56	MG	DA	3491	1/1	0.87	0.08	56,56,56,56	0
56	MG	BA	3502	1/1	0.88	0.13	43,43,43,43	0
56	MG	CA	3062	1/1	0.88	0.28	57,57,57,57	0
56	MG	DA	3069	1/1	0.88	0.09	51,51,51,51	0
56	MG	BA	3724	1/1	0.88	0.12	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3071	1/1	0.88	0.17	55,55,55,55	0
56	MG	BA	3262	1/1	0.88	0.25	56,56,56,56	0
56	MG	AA	3111	1/1	0.88	0.10	95,95,95,95	0
56	MG	BA	3546	1/1	0.88	0.22	48,48,48,48	0
56	MG	DA	3466	1/1	0.88	0.17	56,56,56,56	0
56	MG	BA	3560	1/1	0.88	0.26	61,61,61,61	0
56	MG	BA	3086	1/1	0.88	0.25	49,49,49,49	0
56	MG	AA	3219	1/1	0.88	0.19	57,57,57,57	0
56	MG	DA	3110	1/1	0.88	0.09	49,49,49,49	0
56	MG	BB	3017	1/1	0.88	0.14	64,64,64,64	0
56	MG	AN	101	1/1	0.88	0.10	63,63,63,63	0
56	MG	BA	3164	1/1	0.88	0.22	56,56,56,56	0
56	MG	BN	3001	1/1	0.88	0.26	54,54,54,54	0
56	MG	CA	3111	1/1	0.88	0.15	64,64,64,64	0
56	MG	BA	3597	1/1	0.88	0.20	60,60,60,60	0
56	MG	DA	3127	1/1	0.88	0.10	48,48,48,48	0
56	MG	BA	3165	1/1	0.88	0.20	53,53,53,53	0
56	MG	CA	3124	1/1	0.88	0.10	61,61,61,61	0
56	MG	BQ	205	1/1	0.88	0.13	49,49,49,49	0
56	MG	DA	3519	1/1	0.88	0.09	44,44,44,44	0
56	MG	BA	3608	1/1	0.88	0.07	68,68,68,68	0
56	MG	AA	3004	1/1	0.88	0.20	55,55,55,55	0
56	MG	BA	3173	1/1	0.88	0.29	37,37,37,37	0
56	MG	DA	3543	1/1	0.88	0.12	42,42,42,42	0
56	MG	AA	3048	1/1	0.88	0.15	57,57,57,57	0
56	MG	AA	3052	1/1	0.88	0.25	60,60,60,60	0
56	MG	B7	101	1/1	0.88	0.12	43,43,43,43	0
56	MG	DA	3172	1/1	0.88	0.20	51,51,51,51	0
56	MG	DA	3562	1/1	0.88	0.15	61,61,61,61	0
56	MG	DA	3178	1/1	0.88	0.38	43,43,43,43	0
56	MG	B7	103	1/1	0.88	0.17	48,48,48,48	0
56	MG	B9	502	1/1	0.88	0.19	49,49,49,49	0
56	MG	DA	3566	1/1	0.88	0.30	71,71,71,71	0
56	MG	BA	3104	1/1	0.88	0.28	45,45,45,45	0
56	MG	BA	3620	1/1	0.88	0.14	47,47,47,47	0
56	MG	CA	3008	1/1	0.88	0.25	53,53,53,53	0
56	MG	DA	3218	1/1	0.88	0.09	62,62,62,62	0
56	MG	DA	3221	1/1	0.88	0.26	49,49,49,49	0
56	MG	BA	3192	1/1	0.88	0.12	58,58,58,58	0
56	MG	CA	3018	1/1	0.88	0.10	54,54,54,54	0
56	MG	CA	3019	1/1	0.88	0.14	49,49,49,49	0
56	MG	AA	3012	1/1	0.88	0.07	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3196	1/1	0.88	0.32	56,56,56,56	0
56	MG	BA	3197	1/1	0.88	0.11	39,39,39,39	0
56	MG	AA	3118	1/1	0.88	0.33	52,52,52,52	0
56	MG	CA	3166	1/1	0.88	0.11	59,59,59,59	0
56	MG	DA	3627	1/1	0.88	0.15	43,43,43,43	0
56	MG	CA	3168	1/1	0.88	0.23	77,77,77,77	0
56	MG	BA	3646	1/1	0.88	0.23	52,52,52,52	0
56	MG	CA	3033	1/1	0.88	0.16	68,68,68,68	0
56	MG	BA	3649	1/1	0.88	0.18	66,66,66,66	0
56	MG	BA	3422	1/1	0.88	0.17	42,42,42,42	0
56	MG	DA	3643	1/1	0.88	0.24	53,53,53,53	0
56	MG	BA	3203	1/1	0.88	0.22	32,32,32,32	0
56	MG	AA	3141	1/1	0.88	0.20	48,48,48,48	0
56	MG	AA	3106	1/1	0.88	0.21	56,56,56,56	0
56	MG	DA	3005	1/1	0.88	0.09	42,42,42,42	0
56	MG	AA	3127	1/1	0.88	0.21	62,62,62,62	0
56	MG	DA	3015	1/1	0.88	0.24	49,49,49,49	0
56	MG	CA	3046	1/1	0.88	0.31	53,53,53,53	0
56	MG	BA	3456	1/1	0.88	0.10	52,52,52,52	0
56	MG	AA	3005	1/1	0.88	0.40	66,66,66,66	0
56	MG	BA	3479	1/1	0.88	0.13	56,56,56,56	0
56	MG	DA	3034	1/1	0.88	0.10	40,40,40,40	0
56	MG	AA	3026	1/1	0.88	0.15	41,41,41,41	0
56	MG	AA	3217	1/1	0.88	0.35	67,67,67,67	0
56	MG	CA	3056	1/1	0.88	0.26	64,64,64,64	0
56	MG	BA	3238	1/1	0.88	0.27	51,51,51,51	0
56	MG	BA	3295	1/1	0.89	0.31	75,75,75,75	0
56	MG	AA	3196	1/1	0.89	0.22	65,65,65,65	0
56	MG	DA	3483	1/1	0.89	0.09	49,49,49,49	0
56	MG	BU	201	1/1	0.89	0.36	39,39,39,39	0
56	MG	BU	204	1/1	0.89	0.22	44,44,44,44	0
56	MG	CA	3172	1/1	0.89	0.10	51,51,51,51	0
56	MG	BA	3653	1/1	0.89	0.12	69,69,69,69	0
56	MG	DA	3494	1/1	0.89	0.12	78,78,78,78	0
56	MG	DA	3497	1/1	0.89	0.15	60,60,60,60	0
56	MG	BA	3304	1/1	0.89	0.15	49,49,49,49	0
56	MG	BA	3083	1/1	0.89	0.26	63,63,63,63	0
56	MG	AA	3051	1/1	0.89	0.12	73,73,73,73	0
56	MG	AX	105	1/1	0.89	0.09	56,56,56,56	0
56	MG	AA	3169	1/1	0.89	0.11	76,76,76,76	0
56	MG	DA	3211	1/1	0.89	0.18	51,51,51,51	0
56	MG	DA	3008	1/1	0.89	0.14	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3674	1/1	0.89	0.15	55,55,55,55	0
56	MG	DA	3525	1/1	0.89	0.41	70,70,70,70	0
56	MG	CA	3079	1/1	0.89	0.13	48,48,48,48	0
56	MG	AX	108	1/1	0.89	0.18	61,61,61,61	0
56	MG	DA	3536	1/1	0.89	0.13	80,80,80,80	0
56	MG	BA	3692	1/1	0.89	0.18	36,36,36,36	0
56	MG	CA	3005	1/1	0.89	0.19	54,54,54,54	0
56	MG	DA	3029	1/1	0.89	0.16	61,61,61,61	0
56	MG	CA	3006	1/1	0.89	0.10	77,77,77,77	0
56	MG	BA	3159	1/1	0.89	0.06	48,48,48,48	0
56	MG	DA	3036	1/1	0.89	0.11	35,35,35,35	0
56	MG	BA	3697	1/1	0.89	0.12	78,78,78,78	0
56	MG	BA	3588	1/1	0.89	0.12	48,48,48,48	0
56	MG	CA	3016	1/1	0.89	0.14	76,76,76,76	0
56	MG	DA	3260	1/1	0.89	0.10	40,40,40,40	0
56	MG	DA	3058	1/1	0.89	0.11	47,47,47,47	0
56	MG	BA	3703	1/1	0.89	0.10	31,31,31,31	0
56	MG	DA	3268	1/1	0.89	0.07	40,40,40,40	0
56	MG	DA	3278	1/1	0.89	0.10	47,47,47,47	0
56	MG	CA	3123	1/1	0.89	0.12	77,77,77,77	0
56	MG	DA	3593	1/1	0.89	0.21	73,73,73,73	0
56	MG	BA	3020	1/1	0.89	0.20	45,45,45,45	0
56	MG	DA	3602	1/1	0.89	0.16	52,52,52,52	0
56	MG	DA	3603	1/1	0.89	0.14	55,55,55,55	0
56	MG	BA	3225	1/1	0.89	0.31	62,62,62,62	0
56	MG	BA	3102	1/1	0.89	0.22	52,52,52,52	0
56	MG	AA	3137	1/1	0.89	0.13	42,42,42,42	0
56	MG	CA	3027	1/1	0.89	0.17	57,57,57,57	0
56	MG	CA	3029	1/1	0.89	0.17	59,59,59,59	0
56	MG	CA	3140	1/1	0.89	0.19	73,73,73,73	0
56	MG	BA	3244	1/1	0.89	0.26	65,65,65,65	0
56	MG	AA	3016	1/1	0.89	0.09	63,63,63,63	0
56	MG	DA	3100	1/1	0.89	0.26	56,56,56,56	0
56	MG	BA	3615	1/1	0.89	0.15	36,36,36,36	0
56	MG	DA	3383	1/1	0.89	0.09	56,56,56,56	0
56	MG	DA	3387	1/1	0.89	0.08	56,56,56,56	0
56	MG	BA	3736	1/1	0.89	0.10	48,48,48,48	0
56	MG	BA	3259	1/1	0.89	0.30	27,27,27,27	0
56	MG	BA	3108	1/1	0.89	0.15	55,55,55,55	0
56	MG	DA	3414	1/1	0.89	0.10	49,49,49,49	0
56	MG	DA	3652	1/1	0.89	0.14	60,60,60,60	0
56	MG	AA	3139	1/1	0.89	0.20	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3119	1/1	0.89	0.14	44,44,44,44	0
56	MG	DB	3003	1/1	0.89	0.13	63,63,63,63	0
56	MG	CA	3151	1/1	0.89	0.12	80,80,80,80	0
56	MG	DA	3440	1/1	0.89	0.19	33,33,33,33	0
56	MG	DD	306	1/1	0.89	0.85	44,44,44,44	0
56	MG	DE	303	1/1	0.89	0.14	41,41,41,41	0
56	MG	DA	3450	1/1	0.89	0.09	43,43,43,43	0
56	MG	AA	3081	1/1	0.89	0.23	41,41,41,41	0
56	MG	DA	3455	1/1	0.89	0.13	60,60,60,60	0
56	MG	BA	3464	1/1	0.89	0.07	43,43,43,43	0
56	MG	AA	3033	1/1	0.89	0.24	64,64,64,64	0
56	MG	D3	101	1/1	0.89	0.11	63,63,63,63	0
56	MG	AA	3221	1/1	0.89	0.22	64,64,64,64	0
56	MG	BA	3641	1/1	0.89	0.17	45,45,45,45	0
56	MG	AA	3098	1/1	0.89	0.21	72,72,72,72	0
56	MG	DA	3141	1/1	0.89	0.16	62,62,62,62	0
56	MG	AA	3074	1/1	0.89	0.25	47,47,47,47	0
56	MG	BA	3391	1/1	0.90	0.21	48,48,48,48	0
56	MG	DA	3092	1/1	0.90	0.24	39,39,39,39	0
56	MG	B0	102	1/1	0.90	0.15	40,40,40,40	0
56	MG	DA	3095	1/1	0.90	0.17	61,61,61,61	0
56	MG	DA	3445	1/1	0.90	0.19	39,39,39,39	0
56	MG	BA	3068	1/1	0.90	0.33	54,54,54,54	0
56	MG	DA	3452	1/1	0.90	0.10	56,56,56,56	0
56	MG	DA	3453	1/1	0.90	0.14	61,61,61,61	0
56	MG	AA	3025	1/1	0.90	0.07	69,69,69,69	0
56	MG	BA	3643	1/1	0.90	0.14	43,43,43,43	0
56	MG	DA	3106	1/1	0.90	0.08	41,41,41,41	0
56	MG	BA	3072	1/1	0.90	0.24	45,45,45,45	0
56	MG	CA	3126	1/1	0.90	0.10	61,61,61,61	0
56	MG	AA	3168	1/1	0.90	0.13	68,68,68,68	0
56	MG	DA	3113	1/1	0.90	0.15	43,43,43,43	0
56	MG	CA	3132	1/1	0.90	0.15	70,70,70,70	0
56	MG	DA	3471	1/1	0.90	0.12	37,37,37,37	0
56	MG	DA	3478	1/1	0.90	0.11	46,46,46,46	0
56	MG	AA	3202	1/1	0.90	0.16	76,76,76,76	0
56	MG	AA	3203	1/1	0.90	0.13	63,63,63,63	0
56	MG	BA	3241	1/1	0.90	0.17	63,63,63,63	0
56	MG	BA	3654	1/1	0.90	0.13	25,25,25,25	0
56	MG	AA	3097	1/1	0.90	0.21	43,43,43,43	0
56	MG	DA	3125	1/1	0.90	0.15	48,48,48,48	0
56	MG	BA	3245	1/1	0.90	0.09	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3009	1/1	0.90	0.07	47,47,47,47	0
56	MG	BA	3463	1/1	0.90	0.12	55,55,55,55	0
56	MG	DA	3495	1/1	0.90	0.19	39,39,39,39	0
56	MG	DA	3496	1/1	0.90	0.23	53,53,53,53	0
56	MG	AA	3108	1/1	0.90	0.15	67,67,67,67	0
56	MG	DA	3139	1/1	0.90	0.12	40,40,40,40	0
56	MG	BA	3467	1/1	0.90	0.13	40,40,40,40	0
56	MG	DA	3150	1/1	0.90	0.08	64,64,64,64	0
56	MG	DA	3153	1/1	0.90	0.13	38,38,38,38	0
56	MG	BA	3003	1/1	0.90	0.14	43,43,43,43	0
56	MG	DA	3157	1/1	0.90	0.37	62,62,62,62	0
56	MG	DA	3158	1/1	0.90	0.22	57,57,57,57	0
56	MG	DA	3517	1/1	0.90	0.11	50,50,50,50	0
56	MG	BA	3675	1/1	0.90	0.18	49,49,49,49	0
56	MG	AA	3210	1/1	0.90	0.09	40,40,40,40	0
56	MG	AA	3041	1/1	0.90	0.17	49,49,49,49	0
56	MG	DA	3167	1/1	0.90	0.19	48,48,48,48	0
56	MG	BA	3269	1/1	0.90	0.28	34,34,34,34	0
56	MG	AA	3216	1/1	0.90	0.20	58,58,58,58	0
56	MG	DA	3538	1/1	0.90	0.08	44,44,44,44	0
56	MG	BA	3277	1/1	0.90	0.18	45,45,45,45	0
56	MG	DA	3544	1/1	0.90	0.12	51,51,51,51	0
56	MG	DA	3176	1/1	0.90	0.18	39,39,39,39	0
56	MG	CA	3160	1/1	0.90	0.17	59,59,59,59	0
56	MG	BA	3510	1/1	0.90	0.18	40,40,40,40	0
56	MG	AA	3140	1/1	0.90	0.08	70,70,70,70	0
56	MG	BA	3709	1/1	0.90	0.20	86,86,86,86	0
56	MG	BA	3105	1/1	0.90	0.33	34,34,34,34	0
56	MG	DA	3210	1/1	0.90	0.23	40,40,40,40	0
56	MG	CA	3036	1/1	0.90	0.08	68,68,68,68	0
56	MG	BA	3713	1/1	0.90	0.10	66,66,66,66	0
56	MG	DA	3567	1/1	0.90	0.19	62,62,62,62	0
56	MG	CA	3039	1/1	0.90	0.25	72,72,72,72	0
56	MG	DA	3587	1/1	0.90	0.06	64,64,64,64	0
56	MG	BA	3545	1/1	0.90	0.20	47,47,47,47	0
56	MG	BA	3717	1/1	0.90	0.21	57,57,57,57	0
56	MG	BA	3186	1/1	0.90	0.10	53,53,53,53	0
56	MG	BA	3291	1/1	0.90	0.10	41,41,41,41	0
56	MG	AA	3099	1/1	0.90	0.18	60,60,60,60	0
56	MG	DA	3003	1/1	0.90	0.10	56,56,56,56	0
56	MG	BA	3111	1/1	0.90	0.14	53,53,53,53	0
56	MG	DA	3607	1/1	0.90	0.09	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3296	1/1	0.90	0.23	46,46,46,46	0
56	MG	BA	3112	1/1	0.90	0.10	38,38,38,38	0
56	MG	BB	3001	1/1	0.90	0.16	54,54,54,54	0
56	MG	BA	3298	1/1	0.90	0.09	49,49,49,49	0
56	MG	DA	3022	1/1	0.90	0.10	45,45,45,45	0
56	MG	BB	3004	1/1	0.90	0.18	54,54,54,54	0
56	MG	BA	3044	1/1	0.90	0.20	42,42,42,42	0
56	MG	BA	3048	1/1	0.90	0.15	31,31,31,31	0
56	MG	BA	3601	1/1	0.90	0.27	64,64,64,64	0
56	MG	BA	3604	1/1	0.90	0.19	72,72,72,72	0
56	MG	BD	306	1/1	0.90	0.08	46,46,46,46	0
56	MG	BA	3059	1/1	0.90	0.34	45,45,45,45	0
56	MG	DA	3288	1/1	0.90	0.17	47,47,47,47	0
56	MG	DA	3291	1/1	0.90	0.15	35,35,35,35	0
56	MG	DA	3040	1/1	0.90	0.09	42,42,42,42	0
56	MG	BA	3201	1/1	0.90	0.20	36,36,36,36	0
56	MG	DA	3307	1/1	0.90	0.21	37,37,37,37	0
56	MG	DA	3043	1/1	0.90	0.27	54,54,54,54	0
56	MG	DA	3318	1/1	0.90	0.11	45,45,45,45	0
56	MG	DA	3321	1/1	0.90	0.15	41,41,41,41	0
56	MG	DA	3048	1/1	0.90	0.21	37,37,37,37	0
56	MG	DA	3329	1/1	0.90	0.07	53,53,53,53	0
56	MG	BA	3340	1/1	0.90	0.08	57,57,57,57	0
56	MG	DA	3056	1/1	0.90	0.21	43,43,43,43	0
56	MG	DA	3353	1/1	0.90	0.10	62,62,62,62	0
56	MG	DF	305	1/1	0.90	0.16	39,39,39,39	0
56	MG	AA	3038	1/1	0.90	0.30	66,66,66,66	0
56	MG	AA	3126	1/1	0.90	0.24	54,54,54,54	0
56	MG	AA	3135	1/1	0.90	0.12	41,41,41,41	0
56	MG	DA	3365	1/1	0.90	0.11	40,40,40,40	0
56	MG	CA	3099	1/1	0.90	0.17	65,65,65,65	0
56	MG	BA	3210	1/1	0.90	0.13	34,34,34,34	0
56	MG	BA	3376	1/1	0.90	0.08	48,48,48,48	0
56	MG	BV	201	1/1	0.90	0.17	53,53,53,53	0
56	MG	DA	3078	1/1	0.90	0.10	44,44,44,44	0
56	MG	BA	3384	1/1	0.90	0.17	60,60,60,60	0
56	MG	DA	3053	1/1	0.91	0.11	42,42,42,42	0
56	MG	BA	3719	1/1	0.91	0.08	25,25,25,25	0
56	MG	DA	3216	1/1	0.91	0.16	31,31,31,31	0
56	MG	BA	3127	1/1	0.91	0.16	50,50,50,50	0
56	MG	BA	3129	1/1	0.91	0.14	36,36,36,36	0
56	MG	BA	3731	1/1	0.91	0.12	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3466	1/1	0.91	0.14	61,61,61,61	0
56	MG	BA	3230	1/1	0.91	0.15	46,46,46,46	0
56	MG	DA	3068	1/1	0.91	0.09	55,55,55,55	0
56	MG	BA	3475	1/1	0.91	0.18	36,36,36,36	0
56	MG	CA	3028	1/1	0.91	0.26	43,43,43,43	0
56	MG	BA	3231	1/1	0.91	0.23	38,38,38,38	0
56	MG	BB	3002	1/1	0.91	0.16	59,59,59,59	0
56	MG	DA	3249	1/1	0.91	0.18	28,28,28,28	0
56	MG	BA	3233	1/1	0.91	0.23	47,47,47,47	0
56	MG	BA	3488	1/1	0.91	0.14	35,35,35,35	0
56	MG	DA	3524	1/1	0.91	0.09	28,28,28,28	0
56	MG	DA	3086	1/1	0.91	0.19	43,43,43,43	0
56	MG	BA	3312	1/1	0.91	0.12	58,58,58,58	0
56	MG	DA	3266	1/1	0.91	0.13	43,43,43,43	0
56	MG	DA	3528	1/1	0.91	0.08	56,56,56,56	0
56	MG	BB	3006	1/1	0.91	0.16	39,39,39,39	0
56	MG	AA	3020	1/1	0.91	0.07	77,77,77,77	0
56	MG	DA	3269	1/1	0.91	0.13	48,48,48,48	0
56	MG	BA	3016	1/1	0.91	0.19	33,33,33,33	0
56	MG	BA	3336	1/1	0.91	0.21	54,54,54,54	0
56	MG	DA	3280	1/1	0.91	0.09	57,57,57,57	0
56	MG	BA	3098	1/1	0.91	0.15	35,35,35,35	0
56	MG	DA	3105	1/1	0.91	0.12	48,48,48,48	0
56	MG	BD	312	1/1	0.91	0.24	80,80,80,80	0
56	MG	BE	301	1/1	0.91	0.21	43,43,43,43	0
56	MG	DA	3108	1/1	0.91	0.17	37,37,37,37	0
56	MG	BA	3650	1/1	0.91	0.20	45,45,45,45	0
56	MG	BG	3003	1/1	0.91	0.09	42,42,42,42	0
56	MG	AA	3055	1/1	0.91	0.17	50,50,50,50	0
56	MG	BA	3535	1/1	0.91	0.11	37,37,37,37	0
56	MG	DA	3578	1/1	0.91	0.17	49,49,49,49	0
56	MG	BA	3142	1/1	0.91	0.39	46,46,46,46	0
56	MG	DA	3118	1/1	0.91	0.06	39,39,39,39	0
56	MG	BA	3356	1/1	0.91	0.15	56,56,56,56	0
56	MG	BA	3663	1/1	0.91	0.23	56,56,56,56	0
56	MG	DA	3342	1/1	0.91	0.08	52,52,52,52	0
56	MG	DA	3350	1/1	0.91	0.07	32,32,32,32	0
56	MG	BA	3101	1/1	0.91	0.12	35,35,35,35	0
56	MG	BA	3549	1/1	0.91	0.15	27,27,27,27	0
56	MG	BA	3554	1/1	0.91	0.16	31,31,31,31	0
56	MG	DA	3606	1/1	0.91	0.08	58,58,58,58	0
56	MG	BV	203	1/1	0.91	0.32	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3559	1/1	0.91	0.14	48,48,48,48	0
56	MG	BA	3257	1/1	0.91	0.26	38,38,38,38	0
56	MG	BA	3678	1/1	0.91	0.23	53,53,53,53	0
56	MG	DA	3617	1/1	0.91	0.19	58,58,58,58	0
56	MG	DA	3386	1/1	0.91	0.11	56,56,56,56	0
56	MG	BA	3373	1/1	0.91	0.17	36,36,36,36	0
56	MG	DA	3388	1/1	0.91	0.08	54,54,54,54	0
56	MG	DA	3390	1/1	0.91	0.08	42,42,42,42	0
56	MG	DA	3140	1/1	0.91	0.22	54,54,54,54	0
56	MG	AA	3119	1/1	0.91	0.28	63,63,63,63	0
56	MG	CA	3074	1/1	0.91	0.22	54,54,54,54	0
56	MG	DA	3412	1/1	0.91	0.18	30,30,30,30	0
56	MG	DA	3152	1/1	0.91	0.13	50,50,50,50	0
56	MG	DA	3636	1/1	0.91	0.12	61,61,61,61	0
56	MG	DA	3012	1/1	0.91	0.14	57,57,57,57	0
56	MG	CA	3075	1/1	0.91	0.24	76,76,76,76	0
56	MG	DA	3155	1/1	0.91	0.20	50,50,50,50	0
56	MG	DA	3156	1/1	0.91	0.25	29,29,29,29	0
56	MG	CA	3077	1/1	0.91	0.22	53,53,53,53	0
56	MG	AA	3043	1/1	0.91	0.30	74,74,74,74	0
56	MG	DA	3159	1/1	0.91	0.08	51,51,51,51	0
56	MG	BA	3151	1/1	0.91	0.11	52,52,52,52	0
56	MG	DB	3007	1/1	0.91	0.22	45,45,45,45	0
56	MG	AA	3027	1/1	0.91	0.08	55,55,55,55	0
56	MG	BA	3039	1/1	0.91	0.14	42,42,42,42	0
56	MG	DB	3012	1/1	0.91	0.23	59,59,59,59	0
56	MG	CA	3002	1/1	0.91	0.13	62,62,62,62	0
56	MG	DA	3168	1/1	0.91	0.27	48,48,48,48	0
56	MG	DA	3459	1/1	0.91	0.09	33,33,33,33	0
56	MG	AA	3173	1/1	0.91	0.08	32,32,32,32	0
56	MG	AA	3001	1/1	0.91	0.11	68,68,68,68	0
56	MG	DN	5001	1/1	0.91	0.09	75,75,75,75	0
56	MG	DA	3171	1/1	0.91	0.16	39,39,39,39	0
56	MG	DV	202	1/1	0.91	0.23	63,63,63,63	0
56	MG	BA	3209	1/1	0.91	0.16	40,40,40,40	0
56	MG	BA	3085	1/1	0.91	0.31	48,48,48,48	0
56	MG	BA	3214	1/1	0.91	0.21	53,53,53,53	0
56	MG	AA	3070	1/1	0.91	0.11	75,75,75,75	0
56	MG	CA	3011	1/1	0.91	0.27	42,42,42,42	0
56	MG	DA	3044	1/1	0.91	0.16	46,46,46,46	0
56	MG	BA	3053	1/1	0.91	0.23	39,39,39,39	0
56	MG	DA	3051	1/1	0.91	0.08	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3010	1/1	0.92	0.10	32,32,32,32	0
56	MG	CA	3152	1/1	0.92	0.19	55,55,55,55	0
56	MG	AX	102	1/1	0.92	0.19	74,74,74,74	0
56	MG	BA	3684	1/1	0.92	0.15	58,58,58,58	0
56	MG	BA	3690	1/1	0.92	0.15	53,53,53,53	0
56	MG	AA	3082	1/1	0.92	0.21	39,39,39,39	0
56	MG	DA	3145	1/1	0.92	0.14	65,65,65,65	0
56	MG	DA	3147	1/1	0.92	0.11	53,53,53,53	0
56	MG	DA	3148	1/1	0.92	0.16	47,47,47,47	0
56	MG	BA	3537	1/1	0.92	0.23	31,31,31,31	0
56	MG	BA	3694	1/1	0.92	0.32	56,56,56,56	0
56	MG	BA	3541	1/1	0.92	0.13	30,30,30,30	0
56	MG	CA	3163	1/1	0.92	0.08	65,65,65,65	0
56	MG	AA	3040	1/1	0.92	0.11	55,55,55,55	0
56	MG	BA	3132	1/1	0.92	0.08	35,35,35,35	0
56	MG	BA	3204	1/1	0.92	0.24	25,25,25,25	0
56	MG	BA	3548	1/1	0.92	0.20	50,50,50,50	0
56	MG	BA	3133	1/1	0.92	0.16	32,32,32,32	0
56	MG	BA	3550	1/1	0.92	0.18	45,45,45,45	0
56	MG	BA	3066	1/1	0.92	0.18	44,44,44,44	0
56	MG	BA	3558	1/1	0.92	0.10	35,35,35,35	0
56	MG	AA	3105	1/1	0.92	0.15	46,46,46,46	0
56	MG	CX	102	1/1	0.92	0.11	61,61,61,61	0
56	MG	BA	3313	1/1	0.92	0.16	36,36,36,36	0
56	MG	AA	3011	1/1	0.92	0.34	55,55,55,55	0
56	MG	DA	3002	1/1	0.92	0.26	55,55,55,55	0
56	MG	BA	3211	1/1	0.92	0.16	38,38,38,38	0
56	MG	BA	3728	1/1	0.92	0.22	32,32,32,32	0
56	MG	DA	3007	1/1	0.92	0.15	30,30,30,30	0
56	MG	DA	3181	1/1	0.92	0.17	36,36,36,36	0
56	MG	DA	3504	1/1	0.92	0.07	44,44,44,44	0
56	MG	DA	3509	1/1	0.92	0.14	55,55,55,55	0
56	MG	DA	3183	1/1	0.92	0.12	54,54,54,54	0
56	MG	BA	3139	1/1	0.92	0.18	51,51,51,51	0
56	MG	DA	3512	1/1	0.92	0.33	61,61,61,61	0
56	MG	AA	3184	1/1	0.92	0.07	72,72,72,72	0
56	MG	BA	3591	1/1	0.92	0.14	48,48,48,48	0
56	MG	AA	3211	1/1	0.92	0.15	36,36,36,36	0
56	MG	DA	3521	1/1	0.92	0.12	62,62,62,62	0
56	MG	DA	3522	1/1	0.92	0.10	61,61,61,61	0
56	MG	DA	3208	1/1	0.92	0.17	43,43,43,43	0
56	MG	DA	3016	1/1	0.92	0.23	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3594	1/1	0.92	0.14	42,42,42,42	0
56	MG	BA	3005	1/1	0.92	0.14	36,36,36,36	0
56	MG	DA	3215	1/1	0.92	0.24	29,29,29,29	0
56	MG	CA	3052	1/1	0.92	0.12	39,39,39,39	0
56	MG	BA	3145	1/1	0.92	0.29	38,38,38,38	0
56	MG	BA	3599	1/1	0.92	0.12	46,46,46,46	0
56	MG	BA	3368	1/1	0.92	0.15	35,35,35,35	0
56	MG	DA	3032	1/1	0.92	0.10	46,46,46,46	0
56	MG	BA	3082	1/1	0.92	0.16	41,41,41,41	0
56	MG	DA	3550	1/1	0.92	0.04	53,53,53,53	0
56	MG	BA	3008	1/1	0.92	0.08	50,50,50,50	0
56	MG	AA	3042	1/1	0.92	0.13	44,44,44,44	0
56	MG	BA	3017	1/1	0.92	0.13	44,44,44,44	0
56	MG	BD	305	1/1	0.92	0.20	48,48,48,48	0
56	MG	AA	3159	1/1	0.92	0.18	57,57,57,57	0
56	MG	AA	3086	1/1	0.92	0.07	51,51,51,51	0
56	MG	AA	3077	1/1	0.92	0.30	65,65,65,65	0
56	MG	CA	3072	1/1	0.92	0.19	38,38,38,38	0
56	MG	BE	308	1/1	0.92	0.18	52,52,52,52	0
56	MG	BF	302	1/1	0.92	0.16	46,46,46,46	0
56	MG	BA	3028	1/1	0.92	0.10	48,48,48,48	0
56	MG	DA	3057	1/1	0.92	0.13	52,52,52,52	0
56	MG	CA	3076	1/1	0.92	0.18	40,40,40,40	0
56	MG	DA	3059	1/1	0.92	0.10	46,46,46,46	0
56	MG	DA	3274	1/1	0.92	0.10	52,52,52,52	0
56	MG	BA	3246	1/1	0.92	0.14	46,46,46,46	0
56	MG	DA	3594	1/1	0.92	0.10	47,47,47,47	0
56	MG	BA	3621	1/1	0.92	0.13	74,74,74,74	0
56	MG	AA	3054	1/1	0.92	0.15	45,45,45,45	0
56	MG	DA	3064	1/1	0.92	0.14	50,50,50,50	0
56	MG	DA	3285	1/1	0.92	0.10	55,55,55,55	0
56	MG	CA	3084	1/1	0.92	0.17	64,64,64,64	0
56	MG	CA	3085	1/1	0.92	0.18	43,43,43,43	0
56	MG	DA	3610	1/1	0.92	0.09	54,54,54,54	0
56	MG	BA	3249	1/1	0.92	0.17	40,40,40,40	0
56	MG	BA	3031	1/1	0.92	0.58	41,41,41,41	0
56	MG	DA	3294	1/1	0.92	0.11	47,47,47,47	0
56	MG	DA	3077	1/1	0.92	0.14	50,50,50,50	0
56	MG	BA	3166	1/1	0.92	0.21	59,59,59,59	0
56	MG	BR	201	1/1	0.92	0.20	51,51,51,51	0
56	MG	CA	3108	1/1	0.92	0.13	52,52,52,52	0
56	MG	AA	3197	1/1	0.92	0.07	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3087	1/1	0.92	0.14	49,49,49,49	0
56	MG	DA	3630	1/1	0.92	0.13	40,40,40,40	0
56	MG	DA	3325	1/1	0.92	0.11	36,36,36,36	0
56	MG	DA	3089	1/1	0.92	0.10	57,57,57,57	0
56	MG	BA	3457	1/1	0.92	0.10	57,57,57,57	0
56	MG	AD	502	1/1	0.92	0.22	43,43,43,43	0
56	MG	BA	3043	1/1	0.92	0.16	52,52,52,52	0
56	MG	BW	204	1/1	0.92	0.15	35,35,35,35	0
56	MG	DA	3641	1/1	0.92	0.21	61,61,61,61	0
56	MG	DA	3097	1/1	0.92	0.19	61,61,61,61	0
56	MG	DA	3098	1/1	0.92	0.63	43,43,43,43	0
56	MG	BA	3648	1/1	0.92	0.22	49,49,49,49	0
56	MG	DA	3653	1/1	0.92	0.09	60,60,60,60	0
56	MG	BA	3275	1/1	0.92	0.16	46,46,46,46	0
56	MG	AF	3001	1/1	0.92	0.17	61,61,61,61	0
56	MG	DB	3002	1/1	0.92	0.17	56,56,56,56	0
56	MG	DA	3366	1/1	0.92	0.19	36,36,36,36	0
56	MG	DB	3004	1/1	0.92	0.13	68,68,68,68	0
56	MG	DA	3376	1/1	0.92	0.07	31,31,31,31	0
56	MG	DB	3008	1/1	0.92	0.14	45,45,45,45	0
56	MG	DA	3377	1/1	0.92	0.14	59,59,59,59	0
56	MG	BA	3651	1/1	0.92	0.20	45,45,45,45	0
56	MG	AA	3034	1/1	0.92	0.14	48,48,48,48	0
56	MG	BA	3280	1/1	0.92	0.35	69,69,69,69	0
56	MG	BA	3281	1/1	0.92	0.20	52,52,52,52	0
56	MG	DF	301	1/1	0.92	0.24	32,32,32,32	0
56	MG	BA	3110	1/1	0.92	0.27	55,55,55,55	0
56	MG	DA	3400	1/1	0.92	0.10	42,42,42,42	0
56	MG	BA	3284	1/1	0.92	0.11	54,54,54,54	0
56	MG	BA	3287	1/1	0.92	0.21	53,53,53,53	0
56	MG	DQ	203	1/1	0.92	0.09	57,57,57,57	0
56	MG	BA	3050	1/1	0.92	0.12	21,21,21,21	0
56	MG	DR	201	1/1	0.92	0.24	65,65,65,65	0
56	MG	CA	3004	1/1	0.92	0.09	96,96,96,96	0
56	MG	DW	201	1/1	0.92	0.07	46,46,46,46	0
56	MG	CA	3143	1/1	0.92	0.09	87,87,87,87	0
56	MG	BA	3671	1/1	0.92	0.13	57,57,57,57	0
56	MG	DA	3420	1/1	0.92	0.10	51,51,51,51	0
56	MG	BA	3501	1/1	0.92	0.13	59,59,59,59	0
56	MG	BA	3052	1/1	0.92	0.14	29,29,29,29	0
56	MG	BA	3290	1/1	0.92	0.14	49,49,49,49	0
56	MG	AA	3201	1/1	0.92	0.14	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3447	1/1	0.92	0.06	56,56,56,56	0
56	MG	DA	3441	1/1	0.93	0.24	53,53,53,53	0
56	MG	BA	3030	1/1	0.93	0.23	51,51,51,51	0
56	MG	AA	3028	1/1	0.93	0.21	60,60,60,60	0
56	MG	BY	201	1/1	0.93	0.26	58,58,58,58	0
56	MG	AA	3207	1/1	0.93	0.16	45,45,45,45	0
56	MG	CA	3145	1/1	0.93	0.05	43,43,43,43	0
56	MG	AA	3148	1/1	0.93	0.09	66,66,66,66	0
56	MG	BA	3481	1/1	0.93	0.09	38,38,38,38	0
56	MG	DA	3146	1/1	0.93	0.16	34,34,34,34	0
56	MG	DA	3457	1/1	0.93	0.12	37,37,37,37	0
56	MG	B1	3001	1/1	0.93	0.32	54,54,54,54	0
56	MG	BA	3087	1/1	0.93	0.07	61,61,61,61	0
56	MG	B3	102	1/1	0.93	0.10	59,59,59,59	0
56	MG	DA	3461	1/1	0.93	0.07	41,41,41,41	0
56	MG	B3	103	1/1	0.93	0.23	41,41,41,41	0
56	MG	BA	3484	1/1	0.93	0.15	54,54,54,54	0
56	MG	BA	3660	1/1	0.93	0.19	71,71,71,71	0
56	MG	BA	3138	1/1	0.93	0.17	46,46,46,46	0
56	MG	AA	3181	1/1	0.93	0.17	57,57,57,57	0
56	MG	AA	3058	1/1	0.93	0.18	50,50,50,50	0
56	MG	DA	3480	1/1	0.93	0.09	52,52,52,52	0
56	MG	BA	3666	1/1	0.93	0.15	61,61,61,61	0
56	MG	BA	3668	1/1	0.93	0.10	38,38,38,38	0
56	MG	BA	3498	1/1	0.93	0.09	39,39,39,39	0
56	MG	BA	3047	1/1	0.93	0.10	47,47,47,47	0
56	MG	BA	3672	1/1	0.93	0.21	48,48,48,48	0
56	MG	DA	3489	1/1	0.93	0.05	36,36,36,36	0
56	MG	BA	3292	1/1	0.93	0.08	63,63,63,63	0
56	MG	BA	3097	1/1	0.93	0.20	33,33,33,33	0
56	MG	BA	3509	1/1	0.93	0.09	27,27,27,27	0
56	MG	BA	3294	1/1	0.93	0.22	37,37,37,37	0
56	MG	CA	3012	1/1	0.93	0.06	49,49,49,49	0
56	MG	CA	3013	1/1	0.93	0.06	51,51,51,51	0
56	MG	BA	3680	1/1	0.93	0.19	37,37,37,37	0
56	MG	AA	3158	1/1	0.93	0.12	44,44,44,44	0
56	MG	DA	3180	1/1	0.93	0.29	46,46,46,46	0
56	MG	AA	3080	1/1	0.93	0.13	53,53,53,53	0
56	MG	BA	3686	1/1	0.93	0.09	25,25,25,25	0
56	MG	DA	3184	1/1	0.93	0.18	45,45,45,45	0
56	MG	CA	3020	1/1	0.93	0.14	47,47,47,47	0
56	MG	BA	3100	1/1	0.93	0.29	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3189	1/1	0.93	0.07	55,55,55,55	0
56	MG	DA	3514	1/1	0.93	0.09	39,39,39,39	0
56	MG	DA	3191	1/1	0.93	0.13	47,47,47,47	0
56	MG	BA	3691	1/1	0.93	0.14	49,49,49,49	0
56	MG	DA	3196	1/1	0.93	0.22	44,44,44,44	0
56	MG	DA	3197	1/1	0.93	0.27	36,36,36,36	0
56	MG	BA	3218	1/1	0.93	0.09	62,62,62,62	0
56	MG	AA	3101	1/1	0.93	0.10	56,56,56,56	0
56	MG	BA	3306	1/1	0.93	0.14	48,48,48,48	0
56	MG	BA	3307	1/1	0.93	0.21	33,33,33,33	0
56	MG	BA	3699	1/1	0.93	0.12	56,56,56,56	0
56	MG	DA	3213	1/1	0.93	0.17	44,44,44,44	0
56	MG	DA	3535	1/1	0.93	0.13	33,33,33,33	0
56	MG	CA	3031	1/1	0.93	0.27	53,53,53,53	0
56	MG	BA	3547	1/1	0.93	0.11	31,31,31,31	0
56	MG	AA	3014	1/1	0.93	0.11	28,28,28,28	0
56	MG	BA	3311	1/1	0.93	0.11	42,42,42,42	0
56	MG	BA	3009	1/1	0.93	0.10	25,25,25,25	0
56	MG	BA	3551	1/1	0.93	0.18	25,25,25,25	0
56	MG	DA	3547	1/1	0.93	0.09	41,41,41,41	0
56	MG	CA	3037	1/1	0.93	0.21	67,67,67,67	0
56	MG	DA	3225	1/1	0.93	0.14	45,45,45,45	0
56	MG	BA	3060	1/1	0.93	0.28	40,40,40,40	0
56	MG	DA	3555	1/1	0.93	0.10	41,41,41,41	0
56	MG	BA	3011	1/1	0.93	0.06	37,37,37,37	0
56	MG	DA	3239	1/1	0.93	0.14	39,39,39,39	0
56	MG	BA	3332	1/1	0.93	0.16	39,39,39,39	0
56	MG	BA	3107	1/1	0.93	0.19	40,40,40,40	0
56	MG	CA	3043	1/1	0.93	0.15	49,49,49,49	0
56	MG	BA	3235	1/1	0.93	0.07	47,47,47,47	0
56	MG	DA	3251	1/1	0.93	0.11	54,54,54,54	0
56	MG	DA	3572	1/1	0.93	0.09	53,53,53,53	0
56	MG	BA	3573	1/1	0.93	0.14	56,56,56,56	0
56	MG	BA	3163	1/1	0.93	0.09	50,50,50,50	0
56	MG	DA	3582	1/1	0.93	0.07	52,52,52,52	0
56	MG	AA	3053	1/1	0.93	0.15	49,49,49,49	0
56	MG	DA	3046	1/1	0.93	0.16	56,56,56,56	0
56	MG	BA	3242	1/1	0.93	0.23	48,48,48,48	0
56	MG	BA	3732	1/1	0.93	0.10	61,61,61,61	0
56	MG	AA	3050	1/1	0.93	0.15	63,63,63,63	0
56	MG	BA	3366	1/1	0.93	0.15	63,63,63,63	0
56	MG	DA	3597	1/1	0.93	0.12	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3273	1/1	0.93	0.06	30,30,30,30	0
56	MG	DA	3599	1/1	0.93	0.10	72,72,72,72	0
56	MG	CA	3055	1/1	0.93	0.26	62,62,62,62	0
56	MG	BA	3737	1/1	0.93	0.19	60,60,60,60	0
56	MG	BA	3738	1/1	0.93	0.07	59,59,59,59	0
56	MG	AA	3116	1/1	0.93	0.17	52,52,52,52	0
56	MG	DA	3608	1/1	0.93	0.14	57,57,57,57	0
56	MG	AA	3107	1/1	0.93	0.18	44,44,44,44	0
56	MG	BA	3169	1/1	0.93	0.52	46,46,46,46	0
56	MG	BA	3114	1/1	0.93	0.27	51,51,51,51	0
56	MG	DA	3287	1/1	0.93	0.17	53,53,53,53	0
56	MG	BA	3252	1/1	0.93	0.07	55,55,55,55	0
56	MG	CA	3068	1/1	0.93	0.13	41,41,41,41	0
56	MG	BA	3382	1/1	0.93	0.08	51,51,51,51	0
56	MG	BA	3253	1/1	0.93	0.12	51,51,51,51	0
56	MG	BB	3008	1/1	0.93	0.08	35,35,35,35	0
56	MG	DA	3075	1/1	0.93	0.07	44,44,44,44	0
56	MG	BA	3609	1/1	0.93	0.13	46,46,46,46	0
56	MG	BA	3387	1/1	0.93	0.10	48,48,48,48	0
56	MG	DA	3319	1/1	0.93	0.05	53,53,53,53	0
56	MG	BA	3256	1/1	0.93	0.10	58,58,58,58	0
56	MG	BB	3018	1/1	0.93	0.14	60,60,60,60	0
56	MG	BA	3115	1/1	0.93	0.29	36,36,36,36	0
56	MG	BA	3116	1/1	0.93	0.20	31,31,31,31	0
56	MG	DA	3330	1/1	0.93	0.10	37,37,37,37	0
56	MG	AK	3001	1/1	0.93	0.17	45,45,45,45	0
56	MG	BA	3188	1/1	0.93	0.13	37,37,37,37	0
56	MG	DA	3644	1/1	0.93	0.10	42,42,42,42	0
56	MG	BE	305	1/1	0.93	0.23	42,42,42,42	0
56	MG	BA	3264	1/1	0.93	0.19	30,30,30,30	0
56	MG	CA	3093	1/1	0.93	0.06	53,53,53,53	0
56	MG	BA	3432	1/1	0.93	0.12	60,60,60,60	0
56	MG	DA	3359	1/1	0.93	0.12	46,46,46,46	0
56	MG	DA	3360	1/1	0.93	0.10	41,41,41,41	0
56	MG	BF	304	1/1	0.93	0.15	35,35,35,35	0
56	MG	BA	3268	1/1	0.93	0.23	46,46,46,46	0
56	MG	BA	3624	1/1	0.93	0.19	52,52,52,52	0
56	MG	AA	3175	1/1	0.93	0.14	76,76,76,76	0
56	MG	DB	3009	1/1	0.93	0.27	40,40,40,40	0
56	MG	DA	3367	1/1	0.93	0.07	42,42,42,42	0
56	MG	BA	3631	1/1	0.93	0.09	78,78,78,78	0
56	MG	BA	3446	1/1	0.93	0.08	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DD	302	1/1	0.93	0.15	46,46,46,46	0
56	MG	CA	3113	1/1	0.93	0.10	77,77,77,77	0
56	MG	DE	301	1/1	0.93	0.35	51,51,51,51	0
56	MG	DA	3109	1/1	0.93	0.11	66,66,66,66	0
56	MG	DE	304	1/1	0.93	0.13	41,41,41,41	0
56	MG	BN	3004	1/1	0.93	0.17	66,66,66,66	0
56	MG	BN	3005	1/1	0.93	0.24	52,52,52,52	0
56	MG	BQ	202	1/1	0.93	0.18	28,28,28,28	0
56	MG	DA	3391	1/1	0.93	0.07	41,41,41,41	0
56	MG	DA	3395	1/1	0.93	0.20	34,34,34,34	0
56	MG	DQ	201	1/1	0.93	0.11	48,48,48,48	0
56	MG	BA	3637	1/1	0.93	0.18	33,33,33,33	0
56	MG	BA	3640	1/1	0.93	0.09	60,60,60,60	0
56	MG	BA	3270	1/1	0.93	0.19	50,50,50,50	0
56	MG	DA	3409	1/1	0.93	0.09	32,32,32,32	0
56	MG	DV	203	1/1	0.93	0.21	54,54,54,54	0
56	MG	DV	204	1/1	0.93	0.10	41,41,41,41	0
56	MG	AA	3176	1/1	0.93	0.10	63,63,63,63	0
56	MG	DA	3120	1/1	0.93	0.28	51,51,51,51	0
56	MG	BA	3078	1/1	0.93	0.07	17,17,17,17	0
56	MG	BU	206	1/1	0.93	0.13	60,60,60,60	0
56	MG	CA	3136	1/1	0.93	0.15	45,45,45,45	0
56	MG	BA	3130	1/1	0.93	0.18	43,43,43,43	0
56	MG	DA	3435	1/1	0.93	0.12	46,46,46,46	0
56	MG	DA	3126	1/1	0.93	0.19	43,43,43,43	0
56	MG	BA	3278	1/1	0.93	0.14	34,34,34,34	0
56	MG	DA	3436	1/1	0.94	0.08	62,62,62,62	0
56	MG	CA	3024	1/1	0.94	0.23	65,65,65,65	0
56	MG	AA	3062	1/1	0.94	0.10	32,32,32,32	0
56	MG	CA	3026	1/1	0.94	0.10	52,52,52,52	0
56	MG	DA	3442	1/1	0.94	0.14	40,40,40,40	0
56	MG	BA	3122	1/1	0.94	0.11	52,52,52,52	0
56	MG	BA	3045	1/1	0.94	0.17	34,34,34,34	0
56	MG	BA	3124	1/1	0.94	0.05	39,39,39,39	0
56	MG	CA	3169	1/1	0.94	0.14	57,57,57,57	0
56	MG	AA	3121	1/1	0.94	0.16	51,51,51,51	0
56	MG	BA	3236	1/1	0.94	0.11	36,36,36,36	0
56	MG	BA	3301	1/1	0.94	0.07	56,56,56,56	0
56	MG	DA	3163	1/1	0.94	0.12	39,39,39,39	0
56	MG	BA	3626	1/1	0.94	0.07	43,43,43,43	0
56	MG	CF	3001	1/1	0.94	0.12	55,55,55,55	0
56	MG	BA	3171	1/1	0.94	0.12	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3630	1/1	0.94	0.20	52,52,52,52	0
56	MG	AA	3124	1/1	0.94	0.16	57,57,57,57	0
56	MG	DA	3462	1/1	0.94	0.09	55,55,55,55	0
56	MG	BA	3177	1/1	0.94	0.08	62,62,62,62	0
56	MG	BA	3634	1/1	0.94	0.64	63,63,63,63	0
56	MG	DA	3173	1/1	0.94	0.30	39,39,39,39	0
56	MG	DA	3174	1/1	0.94	0.14	41,41,41,41	0
56	MG	DA	3476	1/1	0.94	0.12	45,45,45,45	0
56	MG	BA	3049	1/1	0.94	0.23	35,35,35,35	0
56	MG	BA	3639	1/1	0.94	0.08	50,50,50,50	0
56	MG	DA	3179	1/1	0.94	0.22	46,46,46,46	0
56	MG	BA	3181	1/1	0.94	0.15	38,38,38,38	0
56	MG	AA	3125	1/1	0.94	0.07	47,47,47,47	0
56	MG	BD	304	1/1	0.94	0.18	58,58,58,58	0
56	MG	AA	3003	1/1	0.94	0.08	63,63,63,63	0
56	MG	BA	3328	1/1	0.94	0.09	42,42,42,42	0
56	MG	BA	3248	1/1	0.94	0.15	43,43,43,43	0
56	MG	DA	3187	1/1	0.94	0.30	59,59,59,59	0
56	MG	DA	3188	1/1	0.94	0.13	47,47,47,47	0
56	MG	AA	3064	1/1	0.94	0.07	79,79,79,79	0
56	MG	BE	304	1/1	0.94	0.08	49,49,49,49	0
56	MG	DA	3193	1/1	0.94	0.14	65,65,65,65	0
56	MG	DA	3021	1/1	0.94	0.20	35,35,35,35	0
56	MG	DA	3498	1/1	0.94	0.07	56,56,56,56	0
56	MG	BA	3251	1/1	0.94	0.15	61,61,61,61	0
56	MG	BA	3515	1/1	0.94	0.08	56,56,56,56	0
56	MG	DA	3202	1/1	0.94	0.14	42,42,42,42	0
56	MG	DA	3206	1/1	0.94	0.18	42,42,42,42	0
56	MG	BA	3523	1/1	0.94	0.13	48,48,48,48	0
56	MG	BA	3530	1/1	0.94	0.14	31,31,31,31	0
56	MG	BF	307	1/1	0.94	0.07	47,47,47,47	0
56	MG	BA	3058	1/1	0.94	0.18	38,38,38,38	0
56	MG	DA	3033	1/1	0.94	0.11	39,39,39,39	0
56	MG	BA	3021	1/1	0.94	0.29	42,42,42,42	0
56	MG	DA	3035	1/1	0.94	0.09	56,56,56,56	0
56	MG	BA	3657	1/1	0.94	0.18	56,56,56,56	0
56	MG	CA	3064	1/1	0.94	0.08	58,58,58,58	0
56	MG	DA	3219	1/1	0.94	0.18	60,60,60,60	0
56	MG	BA	3540	1/1	0.94	0.14	34,34,34,34	0
56	MG	DA	3523	1/1	0.94	0.10	55,55,55,55	0
56	MG	BA	3254	1/1	0.94	0.15	59,59,59,59	0
56	MG	DA	3042	1/1	0.94	0.21	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BN	3003	1/1	0.94	0.11	59,59,59,59	0
56	MG	CA	3069	1/1	0.94	0.20	69,69,69,69	0
56	MG	DA	3227	1/1	0.94	0.15	53,53,53,53	0
56	MG	DA	3534	1/1	0.94	0.15	45,45,45,45	0
56	MG	BA	3255	1/1	0.94	0.11	41,41,41,41	0
56	MG	DA	3229	1/1	0.94	0.04	40,40,40,40	0
56	MG	DA	3233	1/1	0.94	0.08	42,42,42,42	0
56	MG	BA	3662	1/1	0.94	0.18	39,39,39,39	0
56	MG	DA	3539	1/1	0.94	0.11	53,53,53,53	0
56	MG	BO	201	1/1	0.94	0.08	70,70,70,70	0
56	MG	BQ	201	1/1	0.94	0.24	61,61,61,61	0
56	MG	DA	3241	1/1	0.94	0.13	15,15,15,15	0
56	MG	AA	3031	1/1	0.94	0.15	41,41,41,41	0
56	MG	DA	3247	1/1	0.94	0.06	31,31,31,31	0
56	MG	DA	3551	1/1	0.94	0.10	52,52,52,52	0
56	MG	AA	3103	1/1	0.94	0.19	38,38,38,38	0
56	MG	BA	3062	1/1	0.94	0.23	42,42,42,42	0
56	MG	BA	3260	1/1	0.94	0.12	22,22,22,22	0
56	MG	CA	3078	1/1	0.94	0.11	46,46,46,46	0
56	MG	BA	3141	1/1	0.94	0.16	43,43,43,43	0
56	MG	CA	3080	1/1	0.94	0.15	55,55,55,55	0
56	MG	DA	3264	1/1	0.94	0.13	49,49,49,49	0
56	MG	BA	3670	1/1	0.94	0.15	59,59,59,59	0
56	MG	BA	3199	1/1	0.94	0.22	36,36,36,36	0
56	MG	DA	3066	1/1	0.94	0.32	53,53,53,53	0
56	MG	DA	3067	1/1	0.94	0.25	43,43,43,43	0
56	MG	DA	3575	1/1	0.94	0.10	43,43,43,43	0
56	MG	BU	208	1/1	0.94	0.61	56,56,56,56	0
56	MG	DA	3580	1/1	0.94	0.18	46,46,46,46	0
56	MG	DA	3270	1/1	0.94	0.14	36,36,36,36	0
56	MG	BA	3374	1/1	0.94	0.06	44,44,44,44	0
56	MG	DA	3585	1/1	0.94	0.09	62,62,62,62	0
56	MG	DA	3070	1/1	0.94	0.23	44,44,44,44	0
56	MG	CA	3087	1/1	0.94	0.11	41,41,41,41	0
56	MG	DA	3072	1/1	0.94	0.15	41,41,41,41	0
56	MG	DA	3073	1/1	0.94	0.11	44,44,44,44	0
56	MG	CA	3089	1/1	0.94	0.12	52,52,52,52	0
56	MG	CA	3092	1/1	0.94	0.11	47,47,47,47	0
56	MG	DA	3596	1/1	0.94	0.11	67,67,67,67	0
56	MG	AA	3104	1/1	0.94	0.10	37,37,37,37	0
56	MG	CA	3096	1/1	0.94	0.08	60,60,60,60	0
56	MG	BW	201	1/1	0.94	0.21	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3082	1/1	0.94	0.04	19,19,19,19	0
56	MG	DA	3292	1/1	0.94	0.07	37,37,37,37	0
56	MG	BA	3555	1/1	0.94	0.11	53,53,53,53	0
56	MG	CA	3104	1/1	0.94	0.17	62,62,62,62	0
56	MG	DA	3296	1/1	0.94	0.06	31,31,31,31	0
56	MG	DA	3299	1/1	0.94	0.12	40,40,40,40	0
56	MG	AA	3115	1/1	0.94	0.15	48,48,48,48	0
56	MG	DA	3611	1/1	0.94	0.05	42,42,42,42	0
56	MG	BA	3676	1/1	0.94	0.12	51,51,51,51	0
56	MG	DA	3309	1/1	0.94	0.12	33,33,33,33	0
56	MG	DA	3616	1/1	0.94	0.15	62,62,62,62	0
56	MG	DA	3312	1/1	0.94	0.27	43,43,43,43	0
56	MG	DA	3618	1/1	0.94	0.08	39,39,39,39	0
56	MG	DA	3313	1/1	0.94	0.14	52,52,52,52	0
56	MG	BA	3677	1/1	0.94	0.14	67,67,67,67	0
56	MG	DA	3622	1/1	0.94	0.08	55,55,55,55	0
56	MG	B0	101	1/1	0.94	0.11	36,36,36,36	0
56	MG	AA	3066	1/1	0.94	0.21	38,38,38,38	0
56	MG	BA	3386	1/1	0.94	0.14	58,58,58,58	0
56	MG	B0	104	1/1	0.94	0.07	43,43,43,43	0
56	MG	CA	3116	1/1	0.94	0.14	76,76,76,76	0
56	MG	DA	3326	1/1	0.94	0.11	33,33,33,33	0
56	MG	CA	3118	1/1	0.94	0.07	37,37,37,37	0
56	MG	AA	3036	1/1	0.94	0.12	71,71,71,71	0
56	MG	DA	3332	1/1	0.94	0.11	33,33,33,33	0
56	MG	DA	3102	1/1	0.94	0.08	41,41,41,41	0
56	MG	BA	3563	1/1	0.94	0.09	37,37,37,37	0
56	MG	DA	3343	1/1	0.94	0.09	41,41,41,41	0
56	MG	BA	3568	1/1	0.94	0.14	47,47,47,47	0
56	MG	BA	3689	1/1	0.94	0.17	39,39,39,39	0
56	MG	BA	3038	1/1	0.94	0.30	51,51,51,51	0
56	MG	DA	3648	1/1	0.94	0.15	52,52,52,52	0
56	MG	DA	3650	1/1	0.94	0.21	48,48,48,48	0
56	MG	B5	502	1/1	0.94	0.10	54,54,54,54	0
56	MG	CA	3129	1/1	0.94	0.14	45,45,45,45	0
56	MG	BA	3578	1/1	0.94	0.21	54,54,54,54	0
56	MG	CA	3133	1/1	0.94	0.12	49,49,49,49	0
56	MG	BA	3392	1/1	0.94	0.21	56,56,56,56	0
56	MG	BA	3394	1/1	0.94	0.08	49,49,49,49	0
56	MG	BA	3207	1/1	0.94	0.17	35,35,35,35	0
56	MG	DB	3006	1/1	0.94	0.07	42,42,42,42	0
56	MG	BA	3150	1/1	0.94	0.19	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3369	1/1	0.94	0.09	47,47,47,47	0
56	MG	DA	3373	1/1	0.94	0.13	29,29,29,29	0
56	MG	DA	3374	1/1	0.94	0.05	37,37,37,37	0
56	MG	AA	3032	1/1	0.94	0.23	57,57,57,57	0
56	MG	BA	3153	1/1	0.94	0.17	35,35,35,35	0
56	MG	DA	3378	1/1	0.94	0.07	45,45,45,45	0
56	MG	BA	3212	1/1	0.94	0.20	43,43,43,43	0
56	MG	BA	3705	1/1	0.94	0.12	39,39,39,39	0
56	MG	DE	302	1/1	0.94	0.14	44,44,44,44	0
56	MG	BA	3073	1/1	0.94	0.27	41,41,41,41	0
56	MG	BA	3708	1/1	0.94	0.07	40,40,40,40	0
56	MG	BA	3074	1/1	0.94	0.10	42,42,42,42	0
56	MG	DA	3128	1/1	0.94	0.12	52,52,52,52	0
56	MG	DF	304	1/1	0.94	0.15	44,44,44,44	0
56	MG	AA	3008	1/1	0.94	0.16	54,54,54,54	0
56	MG	DA	3396	1/1	0.94	0.11	35,35,35,35	0
56	MG	DA	3398	1/1	0.94	0.14	35,35,35,35	0
56	MG	BA	3603	1/1	0.94	0.05	39,39,39,39	0
56	MG	BA	3041	1/1	0.94	0.23	32,32,32,32	0
56	MG	BA	3607	1/1	0.94	0.35	53,53,53,53	0
56	MG	DA	3404	1/1	0.94	0.11	47,47,47,47	0
56	MG	BA	3450	1/1	0.94	0.17	46,46,46,46	0
56	MG	BA	3007	1/1	0.94	0.05	35,35,35,35	0
56	MG	CA	3155	1/1	0.94	0.08	71,71,71,71	0
56	MG	BA	3117	1/1	0.94	0.24	25,25,25,25	0
56	MG	BA	3227	1/1	0.94	0.23	32,32,32,32	0
56	MG	BA	3228	1/1	0.94	0.14	63,63,63,63	0
56	MG	DA	3423	1/1	0.94	0.07	29,29,29,29	0
56	MG	BA	3616	1/1	0.94	0.13	33,33,33,33	0
58	ZN	B4	3002	1/1	0.94	0.09	165,165,165,165	0
56	MG	DA	3430	1/1	0.94	0.15	55,55,55,55	0
56	MG	DA	3431	1/1	0.94	0.07	41,41,41,41	0
56	MG	DA	3434	1/1	0.94	0.21	49,49,49,49	0
56	MG	DA	3151	1/1	0.94	0.38	60,60,60,60	0
56	MG	BA	3057	1/1	0.95	0.17	35,35,35,35	0
56	MG	BA	3273	1/1	0.95	0.25	42,42,42,42	0
56	MG	DA	3433	1/1	0.95	0.14	48,48,48,48	0
56	MG	BA	3710	1/1	0.95	0.13	48,48,48,48	0
56	MG	BA	3274	1/1	0.95	0.18	52,52,52,52	0
56	MG	BA	3401	1/1	0.95	0.06	42,42,42,42	0
56	MG	DA	3437	1/1	0.95	0.06	49,49,49,49	0
56	MG	CA	3015	1/1	0.95	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3018	1/1	0.95	0.22	40,40,40,40	0
56	MG	CA	3162	1/1	0.95	0.13	46,46,46,46	0
56	MG	DA	3160	1/1	0.95	0.08	44,44,44,44	0
56	MG	DA	3443	1/1	0.95	0.09	53,53,53,53	0
56	MG	DA	3444	1/1	0.95	0.12	43,43,43,43	0
56	MG	CA	3017	1/1	0.95	0.15	42,42,42,42	0
56	MG	DA	3446	1/1	0.95	0.07	52,52,52,52	0
56	MG	AA	3177	1/1	0.95	0.08	80,80,80,80	0
56	MG	CA	3165	1/1	0.95	0.08	40,40,40,40	0
56	MG	BA	3602	1/1	0.95	0.07	35,35,35,35	0
56	MG	DA	3165	1/1	0.95	0.15	44,44,44,44	0
56	MG	CA	3167	1/1	0.95	0.05	78,78,78,78	0
56	MG	AA	3073	1/1	0.95	0.09	46,46,46,46	0
56	MG	AA	3204	1/1	0.95	0.13	54,54,54,54	0
56	MG	BA	3726	1/1	0.95	0.20	47,47,47,47	0
56	MG	AA	3123	1/1	0.95	0.29	39,39,39,39	0
56	MG	BA	3152	1/1	0.95	0.19	46,46,46,46	0
56	MG	BA	3729	1/1	0.95	0.23	46,46,46,46	0
56	MG	BA	3730	1/1	0.95	0.32	45,45,45,45	0
56	MG	DA	3175	1/1	0.95	0.15	40,40,40,40	0
56	MG	AA	3161	1/1	0.95	0.11	72,72,72,72	0
56	MG	BA	3610	1/1	0.95	0.11	40,40,40,40	0
56	MG	BA	3734	1/1	0.95	0.21	45,45,45,45	0
56	MG	DA	3469	1/1	0.95	0.10	47,47,47,47	0
56	MG	BA	3155	1/1	0.95	0.16	57,57,57,57	0
56	MG	CX	104	1/1	0.95	0.10	40,40,40,40	0
56	MG	DA	3182	1/1	0.95	0.13	32,32,32,32	0
56	MG	BA	3285	1/1	0.95	0.13	32,32,32,32	0
56	MG	BA	3448	1/1	0.95	0.08	29,29,29,29	0
56	MG	AA	3208	1/1	0.95	0.14	46,46,46,46	0
56	MG	DA	3004	1/1	0.95	0.05	29,29,29,29	0
56	MG	BA	3452	1/1	0.95	0.13	47,47,47,47	0
56	MG	DA	3006	1/1	0.95	0.08	42,42,42,42	0
56	MG	AA	3015	1/1	0.95	0.06	73,73,73,73	0
56	MG	AA	3188	1/1	0.95	0.15	53,53,53,53	0
56	MG	BA	3461	1/1	0.95	0.10	36,36,36,36	0
56	MG	DA	3194	1/1	0.95	0.08	48,48,48,48	0
56	MG	BA	3069	1/1	0.95	0.20	41,41,41,41	0
56	MG	DA	3014	1/1	0.95	0.06	34,34,34,34	0
56	MG	AA	3142	1/1	0.95	0.10	38,38,38,38	0
56	MG	DA	3199	1/1	0.95	0.03	42,42,42,42	0
56	MG	DA	3200	1/1	0.95	0.11	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3001	1/1	0.95	0.10	69,69,69,69	0
56	MG	BA	3625	1/1	0.95	0.16	51,51,51,51	0
56	MG	DA	3020	1/1	0.95	0.18	52,52,52,52	0
56	MG	AA	3166	1/1	0.95	0.09	48,48,48,48	0
56	MG	DA	3209	1/1	0.95	0.18	41,41,41,41	0
56	MG	DA	3505	1/1	0.95	0.06	65,65,65,65	0
56	MG	CA	3045	1/1	0.95	0.14	54,54,54,54	0
56	MG	BB	3010	1/1	0.95	0.11	40,40,40,40	0
56	MG	BA	3627	1/1	0.95	0.07	50,50,50,50	0
56	MG	DA	3027	1/1	0.95	0.17	39,39,39,39	0
56	MG	DA	3513	1/1	0.95	0.08	49,49,49,49	0
56	MG	BB	3015	1/1	0.95	0.08	37,37,37,37	0
56	MG	AA	3191	1/1	0.95	0.08	71,71,71,71	0
56	MG	BA	3468	1/1	0.95	0.10	30,30,30,30	0
56	MG	BD	301	1/1	0.95	0.10	28,28,28,28	0
56	MG	DA	3220	1/1	0.95	0.09	37,37,37,37	0
56	MG	BD	302	1/1	0.95	0.22	58,58,58,58	0
56	MG	BD	303	1/1	0.95	0.12	42,42,42,42	0
56	MG	BA	3470	1/1	0.95	0.14	54,54,54,54	0
56	MG	BA	3474	1/1	0.95	0.11	42,42,42,42	0
56	MG	CA	3058	1/1	0.95	0.08	40,40,40,40	0
56	MG	DA	3226	1/1	0.95	0.23	50,50,50,50	0
56	MG	CA	3059	1/1	0.95	0.16	51,51,51,51	0
56	MG	DA	3530	1/1	0.95	0.12	49,49,49,49	0
56	MG	DA	3533	1/1	0.95	0.10	68,68,68,68	0
56	MG	BA	3042	1/1	0.95	0.45	47,47,47,47	0
56	MG	BD	310	1/1	0.95	0.11	48,48,48,48	0
56	MG	DA	3232	1/1	0.95	0.20	50,50,50,50	0
56	MG	BD	311	1/1	0.95	0.12	45,45,45,45	0
56	MG	DA	3235	1/1	0.95	0.10	50,50,50,50	0
56	MG	DA	3237	1/1	0.95	0.12	45,45,45,45	0
56	MG	DA	3045	1/1	0.95	0.21	41,41,41,41	0
56	MG	BA	3167	1/1	0.95	0.20	39,39,39,39	0
56	MG	BA	3232	1/1	0.95	0.06	29,29,29,29	0
56	MG	DA	3049	1/1	0.95	0.13	58,58,58,58	0
56	MG	DA	3242	1/1	0.95	0.18	35,35,35,35	0
56	MG	DA	3050	1/1	0.95	0.12	31,31,31,31	0
56	MG	DA	3246	1/1	0.95	0.09	24,24,24,24	0
56	MG	CA	3066	1/1	0.95	0.10	55,55,55,55	0
56	MG	DA	3052	1/1	0.95	0.07	23,23,23,23	0
56	MG	BE	302	1/1	0.95	0.18	33,33,33,33	0
56	MG	BE	303	1/1	0.95	0.11	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3055	1/1	0.95	0.15	48,48,48,48	0
56	MG	DA	3254	1/1	0.95	0.12	30,30,30,30	0
56	MG	BA	3120	1/1	0.95	0.12	51,51,51,51	0
56	MG	BA	3076	1/1	0.95	0.16	41,41,41,41	0
56	MG	BA	3642	1/1	0.95	0.19	51,51,51,51	0
56	MG	BA	3486	1/1	0.95	0.08	38,38,38,38	0
56	MG	BA	3170	1/1	0.95	0.58	48,48,48,48	0
56	MG	DA	3577	1/1	0.95	0.10	44,44,44,44	0
56	MG	AA	3143	1/1	0.95	0.10	45,45,45,45	0
56	MG	BA	3237	1/1	0.95	0.46	51,51,51,51	0
56	MG	BG	3001	1/1	0.95	0.07	64,64,64,64	0
56	MG	DA	3065	1/1	0.95	0.12	38,38,38,38	0
56	MG	DA	3583	1/1	0.95	0.14	48,48,48,48	0
56	MG	DA	3584	1/1	0.95	0.14	61,61,61,61	0
56	MG	BG	3002	1/1	0.95	0.15	42,42,42,42	0
56	MG	BA	3647	1/1	0.95	0.08	34,34,34,34	0
56	MG	DA	3275	1/1	0.95	0.08	38,38,38,38	0
56	MG	BA	3079	1/1	0.95	0.10	42,42,42,42	0
56	MG	BA	3499	1/1	0.95	0.09	55,55,55,55	0
56	MG	BA	3500	1/1	0.95	0.07	37,37,37,37	0
56	MG	BA	3174	1/1	0.95	0.12	48,48,48,48	0
56	MG	BA	3175	1/1	0.95	0.10	48,48,48,48	0
56	MG	BA	3243	1/1	0.95	0.17	48,48,48,48	0
56	MG	BN	3006	1/1	0.95	0.04	24,24,24,24	0
56	MG	CA	3088	1/1	0.95	0.08	43,43,43,43	0
56	MG	DA	3601	1/1	0.95	0.09	77,77,77,77	0
56	MG	DA	3076	1/1	0.95	0.27	44,44,44,44	0
56	MG	BA	3320	1/1	0.95	0.14	57,57,57,57	0
56	MG	CA	3091	1/1	0.95	0.05	72,72,72,72	0
56	MG	DA	3079	1/1	0.95	0.06	37,37,37,37	0
56	MG	DA	3295	1/1	0.95	0.18	39,39,39,39	0
56	MG	BA	3324	1/1	0.95	0.18	36,36,36,36	0
56	MG	DA	3297	1/1	0.95	0.09	57,57,57,57	0
56	MG	BA	3327	1/1	0.95	0.10	38,38,38,38	0
56	MG	CA	3094	1/1	0.95	0.21	43,43,43,43	0
56	MG	DA	3614	1/1	0.95	0.07	48,48,48,48	0
56	MG	DA	3085	1/1	0.95	0.09	36,36,36,36	0
56	MG	BA	3514	1/1	0.95	0.14	37,37,37,37	0
56	MG	DA	3310	1/1	0.95	0.12	53,53,53,53	0
56	MG	CA	3097	1/1	0.95	0.12	48,48,48,48	0
56	MG	DA	3619	1/1	0.95	0.06	48,48,48,48	0
56	MG	BA	3176	1/1	0.95	0.10	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3091	1/1	0.95	0.29	44,44,44,44	0
56	MG	DA	3316	1/1	0.95	0.15	58,58,58,58	0
56	MG	CA	3100	1/1	0.95	0.08	60,60,60,60	0
56	MG	BA	3080	1/1	0.95	0.20	45,45,45,45	0
56	MG	DA	3094	1/1	0.95	0.09	26,26,26,26	0
56	MG	BR	202	1/1	0.95	0.07	27,27,27,27	0
56	MG	DA	3628	1/1	0.95	0.14	63,63,63,63	0
56	MG	AA	3130	1/1	0.95	0.17	46,46,46,46	0
56	MG	CA	3107	1/1	0.95	0.11	60,60,60,60	0
56	MG	DA	3327	1/1	0.95	0.07	29,29,29,29	0
56	MG	DA	3634	1/1	0.95	0.10	51,51,51,51	0
56	MG	AA	3018	1/1	0.95	0.14	38,38,38,38	0
56	MG	BA	3667	1/1	0.95	0.09	63,63,63,63	0
56	MG	DA	3637	1/1	0.95	0.15	48,48,48,48	0
56	MG	BA	3335	1/1	0.95	0.08	35,35,35,35	0
56	MG	DA	3334	1/1	0.95	0.14	49,49,49,49	0
56	MG	DA	3335	1/1	0.95	0.15	38,38,38,38	0
56	MG	BA	3182	1/1	0.95	0.28	51,51,51,51	0
56	MG	DA	3103	1/1	0.95	0.19	48,48,48,48	0
56	MG	DA	3645	1/1	0.95	0.07	30,30,30,30	0
56	MG	DA	3646	1/1	0.95	0.06	38,38,38,38	0
56	MG	DA	3104	1/1	0.95	0.13	62,62,62,62	0
56	MG	DA	3348	1/1	0.95	0.13	37,37,37,37	0
56	MG	DA	3649	1/1	0.95	0.15	24,24,24,24	0
56	MG	BA	3339	1/1	0.95	0.07	43,43,43,43	0
56	MG	DA	3651	1/1	0.95	0.10	52,52,52,52	0
56	MG	BA	3046	1/1	0.95	0.09	29,29,29,29	0
56	MG	BA	3351	1/1	0.95	0.06	30,30,30,30	0
56	MG	BA	3352	1/1	0.95	0.10	34,34,34,34	0
56	MG	BX	3001	1/1	0.95	0.13	55,55,55,55	0
56	MG	BA	3185	1/1	0.95	0.19	47,47,47,47	0
56	MG	DA	3111	1/1	0.95	0.15	53,53,53,53	0
56	MG	DA	3362	1/1	0.95	0.07	41,41,41,41	0
56	MG	BA	3010	1/1	0.95	0.14	32,32,32,32	0
56	MG	BA	3187	1/1	0.95	0.14	50,50,50,50	0
56	MG	DA	3114	1/1	0.95	0.06	37,37,37,37	0
56	MG	BA	3361	1/1	0.95	0.12	34,34,34,34	0
56	MG	DA	3116	1/1	0.95	0.14	39,39,39,39	0
56	MG	DA	3372	1/1	0.95	0.10	45,45,45,45	0
56	MG	BA	3365	1/1	0.95	0.10	20,20,20,20	0
56	MG	BA	3679	1/1	0.95	0.19	27,27,27,27	0
56	MG	CA	3131	1/1	0.95	0.08	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DD	307	1/1	0.95	0.09	38,38,38,38	0
56	MG	AA	3150	1/1	0.95	0.18	46,46,46,46	0
56	MG	BA	3013	1/1	0.95	0.06	40,40,40,40	0
56	MG	DA	3381	1/1	0.95	0.14	47,47,47,47	0
56	MG	BA	3014	1/1	0.95	0.27	34,34,34,34	0
56	MG	DE	305	1/1	0.95	0.23	65,65,65,65	0
56	MG	BA	3093	1/1	0.95	0.06	25,25,25,25	0
56	MG	BA	3194	1/1	0.95	0.07	55,55,55,55	0
56	MG	DF	303	1/1	0.95	0.07	43,43,43,43	0
56	MG	AA	3153	1/1	0.95	0.14	45,45,45,45	0
56	MG	DA	3389	1/1	0.95	0.12	27,27,27,27	0
56	MG	AA	3049	1/1	0.95	0.20	51,51,51,51	0
56	MG	BA	3564	1/1	0.95	0.05	52,52,52,52	0
56	MG	DA	3129	1/1	0.95	0.05	43,43,43,43	0
56	MG	B8	101	1/1	0.95	0.28	49,49,49,49	0
56	MG	DA	3133	1/1	0.95	0.17	33,33,33,33	0
56	MG	DA	3399	1/1	0.95	0.08	41,41,41,41	0
56	MG	DR	202	1/1	0.95	0.12	37,37,37,37	0
56	MG	B8	102	1/1	0.95	0.07	60,60,60,60	0
56	MG	CA	3144	1/1	0.95	0.18	63,63,63,63	0
56	MG	BA	3377	1/1	0.95	0.12	32,32,32,32	0
56	MG	BA	3380	1/1	0.95	0.12	53,53,53,53	0
56	MG	DA	3405	1/1	0.95	0.11	47,47,47,47	0
56	MG	BA	3055	1/1	0.95	0.09	44,44,44,44	0
56	MG	BA	3383	1/1	0.95	0.11	38,38,38,38	0
56	MG	BA	3056	1/1	0.95	0.25	44,44,44,44	0
56	MG	D8	5001	1/1	0.95	0.18	47,47,47,47	0
56	MG	BA	3143	1/1	0.95	0.13	40,40,40,40	0
56	MG	BA	3704	1/1	0.95	0.09	85,85,85,85	0
56	MG	DA	3149	1/1	0.95	0.06	47,47,47,47	0
56	MG	BA	3590	1/1	0.95	0.09	64,64,64,64	0
56	MG	BA	3202	1/1	0.95	0.08	41,41,41,41	0
56	MG	BP	201	1/1	0.96	0.27	40,40,40,40	0
56	MG	BP	202	1/1	0.96	0.08	40,40,40,40	0
56	MG	DA	3136	1/1	0.96	0.05	49,49,49,49	0
56	MG	DA	3507	1/1	0.96	0.13	54,54,54,54	0
56	MG	DA	3508	1/1	0.96	0.12	38,38,38,38	0
56	MG	DA	3137	1/1	0.96	0.21	56,56,56,56	0
56	MG	DA	3138	1/1	0.96	0.15	42,42,42,42	0
56	MG	DA	3009	1/1	0.96	0.05	31,31,31,31	0
56	MG	DA	3011	1/1	0.96	0.10	45,45,45,45	0
56	MG	BP	203	1/1	0.96	0.41	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3142	1/1	0.96	0.23	33,33,33,33	0
56	MG	DA	3143	1/1	0.96	0.07	46,46,46,46	0
56	MG	DA	3516	1/1	0.96	0.05	40,40,40,40	0
56	MG	DA	3298	1/1	0.96	0.13	37,37,37,37	0
56	MG	DA	3144	1/1	0.96	0.19	36,36,36,36	0
56	MG	DA	3520	1/1	0.96	0.07	51,51,51,51	0
56	MG	DA	3302	1/1	0.96	0.10	22,22,22,22	0
56	MG	BP	204	1/1	0.96	0.06	55,55,55,55	0
56	MG	BA	3250	1/1	0.96	0.11	45,45,45,45	0
56	MG	AA	3057	1/1	0.96	0.04	37,37,37,37	0
56	MG	BA	3161	1/1	0.96	0.22	49,49,49,49	0
56	MG	BA	3435	1/1	0.96	0.13	24,24,24,24	0
56	MG	BA	3438	1/1	0.96	0.12	30,30,30,30	0
56	MG	BA	3566	1/1	0.96	0.07	53,53,53,53	0
56	MG	BR	204	1/1	0.96	0.19	43,43,43,43	0
56	MG	DA	3531	1/1	0.96	0.10	57,57,57,57	0
56	MG	DA	3532	1/1	0.96	0.05	57,57,57,57	0
56	MG	BA	3162	1/1	0.96	0.15	23,23,23,23	0
56	MG	BA	3688	1/1	0.96	0.12	54,54,54,54	0
56	MG	BA	3126	1/1	0.96	0.13	24,24,24,24	0
56	MG	DA	3028	1/1	0.96	0.04	35,35,35,35	0
56	MG	BA	3445	1/1	0.96	0.10	25,25,25,25	0
56	MG	AA	3171	1/1	0.96	0.15	72,72,72,72	0
56	MG	BA	3322	1/1	0.96	0.13	22,22,22,22	0
56	MG	DA	3541	1/1	0.96	0.13	35,35,35,35	0
56	MG	DA	3542	1/1	0.96	0.11	32,32,32,32	0
56	MG	DA	3328	1/1	0.96	0.08	28,28,28,28	0
56	MG	BA	3095	1/1	0.96	0.15	55,55,55,55	0
56	MG	AA	3199	1/1	0.96	0.09	88,88,88,88	0
56	MG	BA	3453	1/1	0.96	0.08	18,18,18,18	0
56	MG	DA	3549	1/1	0.96	0.18	52,52,52,52	0
56	MG	DA	3333	1/1	0.96	0.13	58,58,58,58	0
56	MG	BA	3698	1/1	0.96	0.06	41,41,41,41	0
56	MG	BA	3592	1/1	0.96	0.09	28,28,28,28	0
56	MG	BA	3208	1/1	0.96	0.11	41,41,41,41	0
56	MG	BA	3131	1/1	0.96	0.43	54,54,54,54	0
56	MG	AX	107	1/1	0.96	0.05	66,66,66,66	0
56	MG	DA	3558	1/1	0.96	0.09	37,37,37,37	0
56	MG	DA	3559	1/1	0.96	0.12	46,46,46,46	0
56	MG	DA	3560	1/1	0.96	0.05	34,34,34,34	0
56	MG	CA	3095	1/1	0.96	0.09	39,39,39,39	0
56	MG	DA	3349	1/1	0.96	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3167	1/1	0.96	0.08	67,67,67,67	0
56	MG	DA	3351	1/1	0.96	0.14	35,35,35,35	0
56	MG	BA	3019	1/1	0.96	0.09	39,39,39,39	0
56	MG	BA	3707	1/1	0.96	0.09	36,36,36,36	0
56	MG	DA	3569	1/1	0.96	0.14	37,37,37,37	0
56	MG	DA	3571	1/1	0.96	0.12	46,46,46,46	0
56	MG	AA	3122	1/1	0.96	0.33	44,44,44,44	0
56	MG	DA	3358	1/1	0.96	0.15	46,46,46,46	0
56	MG	BA	3338	1/1	0.96	0.16	50,50,50,50	0
56	MG	BA	3002	1/1	0.96	0.23	54,54,54,54	0
56	MG	DA	3579	1/1	0.96	0.09	23,23,23,23	0
56	MG	BA	3711	1/1	0.96	0.09	86,86,86,86	0
56	MG	CA	3106	1/1	0.96	0.16	64,64,64,64	0
56	MG	BA	3022	1/1	0.96	0.15	52,52,52,52	0
56	MG	BA	3345	1/1	0.96	0.09	33,33,33,33	0
56	MG	BA	3473	1/1	0.96	0.06	51,51,51,51	0
56	MG	BA	3271	1/1	0.96	0.21	36,36,36,36	0
56	MG	AA	3193	1/1	0.96	0.10	60,60,60,60	0
56	MG	DA	3588	1/1	0.96	0.07	40,40,40,40	0
56	MG	DA	3589	1/1	0.96	0.10	59,59,59,59	0
56	MG	DA	3370	1/1	0.96	0.12	38,38,38,38	0
56	MG	CA	3112	1/1	0.96	0.10	59,59,59,59	0
56	MG	BA	3476	1/1	0.96	0.08	40,40,40,40	0
56	MG	BA	3721	1/1	0.96	0.07	25,25,25,25	0
56	MG	BA	3219	1/1	0.96	0.07	65,65,65,65	0
56	MG	DA	3595	1/1	0.96	0.09	72,72,72,72	0
56	MG	CA	3117	1/1	0.96	0.12	68,68,68,68	0
56	MG	DA	3063	1/1	0.96	0.05	52,52,52,52	0
56	MG	BA	3004	1/1	0.96	0.08	24,24,24,24	0
56	MG	DA	3192	1/1	0.96	0.11	47,47,47,47	0
56	MG	BA	3355	1/1	0.96	0.12	64,64,64,64	0
56	MG	CA	3120	1/1	0.96	0.10	58,58,58,58	0
56	MG	CA	3121	1/1	0.96	0.23	53,53,53,53	0
56	MG	DA	3604	1/1	0.96	0.10	54,54,54,54	0
56	MG	BA	3106	1/1	0.96	0.18	48,48,48,48	0
56	MG	BA	3357	1/1	0.96	0.07	49,49,49,49	0
56	MG	DA	3198	1/1	0.96	0.15	48,48,48,48	0
56	MG	BA	3358	1/1	0.96	0.06	33,33,33,33	0
56	MG	BA	3489	1/1	0.96	0.09	43,43,43,43	0
56	MG	DA	3201	1/1	0.96	0.06	48,48,48,48	0
56	MG	BA	3490	1/1	0.96	0.07	38,38,38,38	0
56	MG	BA	3494	1/1	0.96	0.16	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3623	1/1	0.96	0.08	47,47,47,47	0
56	MG	BA	3360	1/1	0.96	0.09	38,38,38,38	0
56	MG	BA	3226	1/1	0.96	0.20	32,32,32,32	0
56	MG	BA	3497	1/1	0.96	0.12	62,62,62,62	0
56	MG	DA	3408	1/1	0.96	0.17	37,37,37,37	0
56	MG	BA	3178	1/1	0.96	0.11	48,48,48,48	0
56	MG	BA	3279	1/1	0.96	0.21	48,48,48,48	0
56	MG	BA	3629	1/1	0.96	0.12	47,47,47,47	0
56	MG	AA	3160	1/1	0.96	0.17	52,52,52,52	0
56	MG	AM	3001	1/1	0.96	0.04	65,65,65,65	0
56	MG	DA	3419	1/1	0.96	0.07	31,31,31,31	0
56	MG	DA	3217	1/1	0.96	0.23	54,54,54,54	0
56	MG	DA	3422	1/1	0.96	0.06	38,38,38,38	0
56	MG	AA	3213	1/1	0.96	0.07	29,29,29,29	0
56	MG	BA	3633	1/1	0.96	0.07	58,58,58,58	0
56	MG	DA	3428	1/1	0.96	0.18	51,51,51,51	0
56	MG	DA	3429	1/1	0.96	0.17	44,44,44,44	0
56	MG	BA	3504	1/1	0.96	0.17	41,41,41,41	0
56	MG	DA	3088	1/1	0.96	0.04	46,46,46,46	0
56	MG	DA	3432	1/1	0.96	0.10	66,66,66,66	0
56	MG	BA	3505	1/1	0.96	0.10	59,59,59,59	0
56	MG	BA	3638	1/1	0.96	0.09	37,37,37,37	0
56	MG	BA	3506	1/1	0.96	0.08	30,30,30,30	0
56	MG	AA	3214	1/1	0.96	0.13	75,75,75,75	0
56	MG	BB	3016	1/1	0.96	0.15	21,21,21,21	0
56	MG	BA	3508	1/1	0.96	0.17	34,34,34,34	0
56	MG	BA	3034	1/1	0.96	0.27	52,52,52,52	0
56	MG	BA	3113	1/1	0.96	0.14	32,32,32,32	0
56	MG	DA	3230	1/1	0.96	0.12	62,62,62,62	0
56	MG	BA	3084	1/1	0.96	0.12	33,33,33,33	0
56	MG	BA	3513	1/1	0.96	0.06	45,45,45,45	0
56	MG	BA	3035	1/1	0.96	0.04	37,37,37,37	0
56	MG	DA	3236	1/1	0.96	0.15	46,46,46,46	0
56	MG	BA	3036	1/1	0.96	0.12	38,38,38,38	0
56	MG	DA	3449	1/1	0.96	0.08	43,43,43,43	0
56	MG	BA	3521	1/1	0.96	0.09	49,49,49,49	0
56	MG	BD	309	1/1	0.96	0.13	42,42,42,42	0
56	MG	BA	3522	1/1	0.96	0.09	49,49,49,49	0
56	MG	BA	3190	1/1	0.96	0.07	42,42,42,42	0
56	MG	DB	3005	1/1	0.96	0.19	43,43,43,43	0
56	MG	BA	3527	1/1	0.96	0.09	64,64,64,64	0
56	MG	BA	3528	1/1	0.96	0.13	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3244	1/1	0.96	0.18	29,29,29,29	0
56	MG	BA	3240	1/1	0.96	0.16	28,28,28,28	0
56	MG	BA	3385	1/1	0.96	0.07	26,26,26,26	0
56	MG	BA	3536	1/1	0.96	0.09	27,27,27,27	0
56	MG	BA	3659	1/1	0.96	0.15	46,46,46,46	0
56	MG	BA	3191	1/1	0.96	0.06	52,52,52,52	0
56	MG	DD	304	1/1	0.96	0.16	35,35,35,35	0
56	MG	BA	3037	1/1	0.96	0.15	31,31,31,31	0
56	MG	DA	3253	1/1	0.96	0.10	42,42,42,42	0
56	MG	DD	308	1/1	0.96	0.05	55,55,55,55	0
56	MG	CA	3051	1/1	0.96	0.09	63,63,63,63	0
56	MG	DA	3467	1/1	0.96	0.04	35,35,35,35	0
56	MG	DA	3468	1/1	0.96	0.07	48,48,48,48	0
56	MG	BA	3154	1/1	0.96	0.09	61,61,61,61	0
56	MG	DA	3470	1/1	0.96	0.12	52,52,52,52	0
56	MG	BA	3542	1/1	0.96	0.16	19,19,19,19	0
56	MG	DA	3473	1/1	0.96	0.21	32,32,32,32	0
56	MG	AA	3215	1/1	0.96	0.09	53,53,53,53	0
56	MG	AA	3186	1/1	0.96	0.05	49,49,49,49	0
56	MG	BA	3398	1/1	0.96	0.08	41,41,41,41	0
56	MG	BA	3121	1/1	0.96	0.20	57,57,57,57	0
56	MG	BA	3090	1/1	0.96	0.12	46,46,46,46	0
56	MG	DO	5001	1/1	0.96	0.08	35,35,35,35	0
56	MG	BA	3404	1/1	0.96	0.13	35,35,35,35	0
56	MG	CA	3060	1/1	0.96	0.25	43,43,43,43	0
56	MG	DQ	204	1/1	0.96	0.12	43,43,43,43	0
56	MG	DA	3272	1/1	0.96	0.12	27,27,27,27	0
56	MG	DA	3485	1/1	0.96	0.05	38,38,38,38	0
56	MG	BA	3091	1/1	0.96	0.25	45,45,45,45	0
56	MG	DA	3488	1/1	0.96	0.05	46,46,46,46	0
56	MG	BA	3408	1/1	0.96	0.07	24,24,24,24	0
56	MG	DA	3490	1/1	0.96	0.08	39,39,39,39	0
56	MG	BA	3409	1/1	0.96	0.13	27,27,27,27	0
56	MG	DA	3276	1/1	0.96	0.07	36,36,36,36	0
56	MG	BA	3415	1/1	0.96	0.14	27,27,27,27	0
56	MG	DA	3130	1/1	0.96	0.09	32,32,32,32	0
56	MG	BA	3557	1/1	0.96	0.16	31,31,31,31	0
56	MG	DA	3281	1/1	0.96	0.12	42,42,42,42	0
56	MG	DA	3282	1/1	0.96	0.07	36,36,36,36	0
58	ZN	D4	501	1/1	0.96	0.11	153,153,153,153	0
56	MG	DA	3283	1/1	0.96	0.06	33,33,33,33	0
56	MG	DA	3132	1/1	0.96	0.21	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3501	1/1	0.96	0.11	23,23,23,23	0
56	MG	BA	3200	1/1	0.96	0.13	25,25,25,25	0
56	MG	BA	3333	1/1	0.97	0.16	49,49,49,49	0
56	MG	BA	3538	1/1	0.97	0.08	36,36,36,36	0
56	MG	BA	3652	1/1	0.97	0.14	64,64,64,64	0
56	MG	DA	3010	1/1	0.97	0.06	39,39,39,39	0
56	MG	BA	3539	1/1	0.97	0.09	35,35,35,35	0
56	MG	BA	3032	1/1	0.97	0.13	49,49,49,49	0
56	MG	BE	306	1/1	0.97	0.15	46,46,46,46	0
56	MG	DA	3323	1/1	0.97	0.06	30,30,30,30	0
56	MG	DA	3324	1/1	0.97	0.17	40,40,40,40	0
56	MG	BE	307	1/1	0.97	0.17	39,39,39,39	0
56	MG	BA	3655	1/1	0.97	0.10	52,52,52,52	0
56	MG	BE	310	1/1	0.97	0.08	50,50,50,50	0
56	MG	DA	3017	1/1	0.97	0.07	46,46,46,46	0
56	MG	DA	3529	1/1	0.97	0.12	63,63,63,63	0
56	MG	BA	3433	1/1	0.97	0.14	39,39,39,39	0
56	MG	BF	303	1/1	0.97	0.12	36,36,36,36	0
56	MG	BA	3172	1/1	0.97	0.44	48,48,48,48	0
56	MG	BF	305	1/1	0.97	0.09	35,35,35,35	0
56	MG	BF	306	1/1	0.97	0.09	37,37,37,37	0
56	MG	BA	3012	1/1	0.97	0.11	40,40,40,40	0
56	MG	DA	3339	1/1	0.97	0.07	37,37,37,37	0
56	MG	DA	3166	1/1	0.97	0.05	32,32,32,32	0
56	MG	DA	3025	1/1	0.97	0.27	44,44,44,44	0
56	MG	BA	3439	1/1	0.97	0.07	34,34,34,34	0
56	MG	DA	3344	1/1	0.97	0.07	26,26,26,26	0
56	MG	DA	3346	1/1	0.97	0.11	29,29,29,29	0
56	MG	BA	3054	1/1	0.97	0.21	46,46,46,46	0
56	MG	BA	3239	1/1	0.97	0.11	33,33,33,33	0
56	MG	BA	3148	1/1	0.97	0.24	52,52,52,52	0
56	MG	DA	3546	1/1	0.97	0.13	44,44,44,44	0
56	MG	DA	3031	1/1	0.97	0.10	55,55,55,55	0
56	MG	BA	3341	1/1	0.97	0.04	33,33,33,33	0
56	MG	BA	3665	1/1	0.97	0.10	39,39,39,39	0
56	MG	AA	3185	1/1	0.97	0.15	46,46,46,46	0
56	MG	DA	3552	1/1	0.97	0.06	34,34,34,34	0
56	MG	BA	3449	1/1	0.97	0.06	21,21,21,21	0
56	MG	BA	3552	1/1	0.97	0.17	29,29,29,29	0
56	MG	DA	3038	1/1	0.97	0.07	39,39,39,39	0
56	MG	BA	3346	1/1	0.97	0.09	37,37,37,37	0
56	MG	BA	3451	1/1	0.97	0.11	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3347	1/1	0.97	0.08	25,25,25,25	0
56	MG	DA	3364	1/1	0.97	0.06	32,32,32,32	0
56	MG	BA	3349	1/1	0.97	0.12	43,43,43,43	0
56	MG	BA	3454	1/1	0.97	0.06	22,22,22,22	0
56	MG	CA	3082	1/1	0.97	0.05	47,47,47,47	0
56	MG	CA	3083	1/1	0.97	0.07	39,39,39,39	0
56	MG	BA	3455	1/1	0.97	0.09	47,47,47,47	0
56	MG	DA	3371	1/1	0.97	0.05	44,44,44,44	0
56	MG	AA	3151	1/1	0.97	0.05	41,41,41,41	0
56	MG	DA	3570	1/1	0.97	0.14	28,28,28,28	0
56	MG	BA	3125	1/1	0.97	0.10	39,39,39,39	0
56	MG	BA	3458	1/1	0.97	0.06	29,29,29,29	0
56	MG	DA	3573	1/1	0.97	0.11	40,40,40,40	0
56	MG	DA	3574	1/1	0.97	0.09	56,56,56,56	0
56	MG	DA	3375	1/1	0.97	0.08	60,60,60,60	0
56	MG	DA	3576	1/1	0.97	0.08	38,38,38,38	0
56	MG	BA	3283	1/1	0.97	0.08	17,17,17,17	0
56	MG	AA	3172	1/1	0.97	0.08	53,53,53,53	0
56	MG	BA	3571	1/1	0.97	0.06	65,65,65,65	0
56	MG	BA	3682	1/1	0.97	0.11	38,38,38,38	0
56	MG	AA	3146	1/1	0.97	0.10	48,48,48,48	0
56	MG	DA	3385	1/1	0.97	0.07	35,35,35,35	0
56	MG	BA	3574	1/1	0.97	0.07	54,54,54,54	0
56	MG	BU	202	1/1	0.97	0.23	32,32,32,32	0
56	MG	BU	203	1/1	0.97	0.07	33,33,33,33	0
56	MG	DA	3586	1/1	0.97	0.03	29,29,29,29	0
56	MG	BA	3576	1/1	0.97	0.13	23,23,23,23	0
56	MG	BA	3577	1/1	0.97	0.07	52,52,52,52	0
56	MG	BU	207	1/1	0.97	0.11	40,40,40,40	0
56	MG	DA	3393	1/1	0.97	0.10	41,41,41,41	0
56	MG	DA	3203	1/1	0.97	0.08	41,41,41,41	0
56	MG	DA	3204	1/1	0.97	0.22	34,34,34,34	0
56	MG	DA	3205	1/1	0.97	0.09	38,38,38,38	0
56	MG	CA	3101	1/1	0.97	0.07	70,70,70,70	0
56	MG	CA	3102	1/1	0.97	0.05	41,41,41,41	0
56	MG	BA	3286	1/1	0.97	0.14	32,32,32,32	0
56	MG	BA	3465	1/1	0.97	0.07	40,40,40,40	0
56	MG	DA	3403	1/1	0.97	0.07	28,28,28,28	0
56	MG	AA	3174	1/1	0.97	0.10	33,33,33,33	0
56	MG	BA	3582	1/1	0.97	0.12	25,25,25,25	0
56	MG	BW	203	1/1	0.97	0.16	45,45,45,45	0
56	MG	BA	3584	1/1	0.97	0.11	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3214	1/1	0.97	0.10	64,64,64,64	0
56	MG	BA	3587	1/1	0.97	0.12	23,23,23,23	0
56	MG	AA	3163	1/1	0.97	0.08	28,28,28,28	0
56	MG	BA	3589	1/1	0.97	0.09	51,51,51,51	0
56	MG	DA	3416	1/1	0.97	0.04	44,44,44,44	0
56	MG	BA	3184	1/1	0.97	0.11	49,49,49,49	0
56	MG	AA	3154	1/1	0.97	0.08	63,63,63,63	0
56	MG	DA	3421	1/1	0.97	0.15	34,34,34,34	0
56	MG	BA	3702	1/1	0.97	0.06	56,56,56,56	0
56	MG	BA	3471	1/1	0.97	0.18	51,51,51,51	0
56	MG	DA	3424	1/1	0.97	0.07	30,30,30,30	0
56	MG	DA	3426	1/1	0.97	0.15	74,74,74,74	0
56	MG	BA	3364	1/1	0.97	0.08	29,29,29,29	0
56	MG	AA	3092	1/1	0.97	0.27	50,50,50,50	0
56	MG	BA	3109	1/1	0.97	0.04	36,36,36,36	0
56	MG	BA	3367	1/1	0.97	0.04	50,50,50,50	0
56	MG	DA	3081	1/1	0.97	0.14	48,48,48,48	0
56	MG	AA	3157	1/1	0.97	0.04	35,35,35,35	0
56	MG	BA	3600	1/1	0.97	0.06	47,47,47,47	0
56	MG	BA	3006	1/1	0.97	0.05	42,42,42,42	0
56	MG	BA	3220	1/1	0.97	0.09	57,57,57,57	0
56	MG	BA	3483	1/1	0.97	0.06	53,53,53,53	0
56	MG	B7	104	1/1	0.97	0.07	51,51,51,51	0
56	MG	BA	3025	1/1	0.97	0.07	28,28,28,28	0
56	MG	BA	3605	1/1	0.97	0.13	59,59,59,59	0
56	MG	DA	3633	1/1	0.97	0.14	54,54,54,54	0
56	MG	BA	3715	1/1	0.97	0.06	47,47,47,47	0
56	MG	BA	3606	1/1	0.97	0.14	25,25,25,25	0
56	MG	CA	3134	1/1	0.97	0.06	82,82,82,82	0
56	MG	BA	3222	1/1	0.97	0.19	25,25,25,25	0
56	MG	BA	3375	1/1	0.97	0.13	31,31,31,31	0
56	MG	CA	3137	1/1	0.97	0.08	48,48,48,48	0
56	MG	BA	3720	1/1	0.97	0.11	33,33,33,33	0
56	MG	DA	3642	1/1	0.97	0.06	35,35,35,35	0
56	MG	DA	3448	1/1	0.97	0.14	57,57,57,57	0
56	MG	BA	3223	1/1	0.97	0.23	47,47,47,47	0
56	MG	BA	3299	1/1	0.97	0.11	9,9,9,9	0
56	MG	BA	3379	1/1	0.97	0.12	22,22,22,22	0
56	MG	BA	3258	1/1	0.97	0.23	40,40,40,40	0
56	MG	BA	3303	1/1	0.97	0.07	35,35,35,35	0
56	MG	BA	3224	1/1	0.97	0.29	64,64,64,64	0
56	MG	BA	3305	1/1	0.97	0.10	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3137	1/1	0.97	0.10	42,42,42,42	0
56	MG	AA	3075	1/1	0.97	0.09	52,52,52,52	0
56	MG	DA	3255	1/1	0.97	0.11	40,40,40,40	0
56	MG	BA	3733	1/1	0.97	0.07	27,27,27,27	0
56	MG	DA	3257	1/1	0.97	0.05	48,48,48,48	0
56	MG	DA	3258	1/1	0.97	0.11	32,32,32,32	0
56	MG	DA	3463	1/1	0.97	0.11	43,43,43,43	0
56	MG	DA	3259	1/1	0.97	0.15	47,47,47,47	0
56	MG	BA	3308	1/1	0.97	0.06	44,44,44,44	0
56	MG	DA	3261	1/1	0.97	0.10	35,35,35,35	0
56	MG	BA	3388	1/1	0.97	0.12	34,34,34,34	0
56	MG	BA	3503	1/1	0.97	0.10	31,31,31,31	0
56	MG	BA	3389	1/1	0.97	0.06	48,48,48,48	0
56	MG	AA	3149	1/1	0.97	0.08	50,50,50,50	0
56	MG	CA	3154	1/1	0.97	0.11	49,49,49,49	0
56	MG	DA	3472	1/1	0.97	0.07	36,36,36,36	0
56	MG	DD	301	1/1	0.97	0.08	46,46,46,46	0
56	MG	BA	3070	1/1	0.97	0.13	35,35,35,35	0
56	MG	DD	303	1/1	0.97	0.08	19,19,19,19	0
56	MG	DA	3474	1/1	0.97	0.05	61,61,61,61	0
56	MG	BA	3265	1/1	0.97	0.13	20,20,20,20	0
56	MG	DA	3477	1/1	0.97	0.06	49,49,49,49	0
56	MG	BA	3397	1/1	0.97	0.07	28,28,28,28	0
56	MG	BA	3266	1/1	0.97	0.19	46,46,46,46	0
56	MG	BA	3314	1/1	0.97	0.10	24,24,24,24	0
56	MG	DA	3121	1/1	0.97	0.07	48,48,48,48	0
56	MG	BA	3267	1/1	0.97	0.13	41,41,41,41	0
56	MG	BA	3512	1/1	0.97	0.12	40,40,40,40	0
56	MG	BA	3195	1/1	0.97	0.09	47,47,47,47	0
56	MG	AA	3198	1/1	0.97	0.06	87,87,87,87	0
56	MG	BA	3326	1/1	0.97	0.12	41,41,41,41	0
56	MG	BB	3012	1/1	0.97	0.08	56,56,56,56	0
56	MG	BB	3013	1/1	0.97	0.06	39,39,39,39	0
56	MG	BA	3635	1/1	0.97	0.07	78,78,78,78	0
56	MG	BA	3636	1/1	0.97	0.06	36,36,36,36	0
56	MG	BA	3517	1/1	0.97	0.10	49,49,49,49	0
56	MG	DA	3493	1/1	0.97	0.08	29,29,29,29	0
56	MG	DQ	202	1/1	0.97	0.14	34,34,34,34	0
56	MG	BA	3518	1/1	0.97	0.08	41,41,41,41	0
56	MG	AA	3183	1/1	0.97	0.09	42,42,42,42	0
56	MG	DA	3290	1/1	0.97	0.05	42,42,42,42	0
56	MG	BA	3118	1/1	0.97	0.11	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3040	1/1	0.97	0.19	42,42,42,42	0
56	MG	DV	201	1/1	0.97	0.08	55,55,55,55	0
56	MG	CE	3002	1/1	0.97	0.06	55,55,55,55	0
56	MG	BA	3416	1/1	0.97	0.25	42,42,42,42	0
56	MG	BA	3524	1/1	0.97	0.21	55,55,55,55	0
56	MG	BA	3525	1/1	0.97	0.13	43,43,43,43	0
56	MG	BA	3526	1/1	0.97	0.08	19,19,19,19	0
56	MG	DY	502	1/1	0.97	0.09	60,60,60,60	0
56	MG	BA	3417	1/1	0.97	0.11	18,18,18,18	0
56	MG	BD	307	1/1	0.97	0.07	43,43,43,43	0
56	MG	BD	308	1/1	0.97	0.16	23,23,23,23	0
56	MG	D5	102	1/1	0.97	0.18	55,55,55,55	0
56	MG	BA	3419	1/1	0.97	0.08	24,24,24,24	0
56	MG	DA	3305	1/1	0.97	0.06	33,33,33,33	0
58	ZN	CN	501	1/1	0.97	0.04	108,108,108,108	0
56	MG	BA	3272	1/1	0.97	0.17	7,7,7,7	0
56	MG	CA	3050	1/1	0.97	0.10	43,43,43,43	0
56	MG	AA	3145	1/1	0.97	0.11	63,63,63,63	0
56	MG	DA	3311	1/1	0.97	0.09	32,32,32,32	0
56	MG	BA	3427	1/1	0.97	0.09	48,48,48,48	0
56	MG	BA	3063	1/1	0.98	0.18	43,43,43,43	0
56	MG	BA	3064	1/1	0.98	0.08	39,39,39,39	0
56	MG	AA	3220	1/1	0.98	0.05	40,40,40,40	0
56	MG	DA	3417	1/1	0.98	0.11	34,34,34,34	0
56	MG	BA	3217	1/1	0.98	0.07	28,28,28,28	0
56	MG	BA	3033	1/1	0.98	0.16	35,35,35,35	0
56	MG	BA	3519	1/1	0.98	0.10	39,39,39,39	0
56	MG	CA	3122	1/1	0.98	0.13	47,47,47,47	0
56	MG	BA	3149	1/1	0.98	0.11	40,40,40,40	0
56	MG	DA	3277	1/1	0.98	0.12	49,49,49,49	0
56	MG	DA	3425	1/1	0.98	0.05	27,27,27,27	0
56	MG	BA	3685	1/1	0.98	0.07	67,67,67,67	0
56	MG	CA	3023	1/1	0.98	0.06	37,37,37,37	0
56	MG	BA	3128	1/1	0.98	0.08	40,40,40,40	0
56	MG	BA	3687	1/1	0.98	0.15	38,38,38,38	0
56	MG	CA	3128	1/1	0.98	0.09	41,41,41,41	0
56	MG	AA	3078	1/1	0.98	0.21	42,42,42,42	0
56	MG	CA	3130	1/1	0.98	0.06	65,65,65,65	0
56	MG	BE	309	1/1	0.98	0.12	25,25,25,25	0
56	MG	AA	3179	1/1	0.98	0.18	34,34,34,34	0
56	MG	BF	301	1/1	0.98	0.18	45,45,45,45	0
56	MG	BA	3051	1/1	0.98	0.09	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3348	1/1	0.98	0.06	64,64,64,64	0
56	MG	BA	3390	1/1	0.98	0.09	30,30,30,30	0
56	MG	DA	3439	1/1	0.98	0.09	28,28,28,28	0
56	MG	BA	3459	1/1	0.98	0.12	31,31,31,31	0
56	MG	BA	3612	1/1	0.98	0.07	37,37,37,37	0
56	MG	BA	3696	1/1	0.98	0.10	39,39,39,39	0
56	MG	BA	3529	1/1	0.98	0.13	35,35,35,35	0
56	MG	DA	3177	1/1	0.98	0.06	33,33,33,33	0
56	MG	BA	3614	1/1	0.98	0.16	30,30,30,30	0
56	MG	AA	3187	1/1	0.98	0.04	62,62,62,62	0
56	MG	BA	3532	1/1	0.98	0.12	34,34,34,34	0
56	MG	DA	3301	1/1	0.98	0.13	45,45,45,45	0
56	MG	BA	3701	1/1	0.98	0.10	32,32,32,32	0
56	MG	BA	3533	1/1	0.98	0.07	32,32,32,32	0
56	MG	DA	3451	1/1	0.98	0.05	49,49,49,49	0
56	MG	DA	3304	1/1	0.98	0.07	35,35,35,35	0
56	MG	AA	3205	1/1	0.98	0.10	61,61,61,61	0
56	MG	DA	3306	1/1	0.98	0.08	33,33,33,33	0
56	MG	DA	3605	1/1	0.98	0.05	44,44,44,44	0
56	MG	BA	3393	1/1	0.98	0.06	38,38,38,38	0
56	MG	DA	3308	1/1	0.98	0.06	30,30,30,30	0
56	MG	AX	110	1/1	0.98	0.14	42,42,42,42	0
56	MG	BA	3395	1/1	0.98	0.09	25,25,25,25	0
56	MG	BA	3179	1/1	0.98	0.11	43,43,43,43	0
56	MG	BA	3024	1/1	0.98	0.19	35,35,35,35	0
56	MG	BA	3399	1/1	0.98	0.14	18,18,18,18	0
56	MG	BA	3469	1/1	0.98	0.05	38,38,38,38	0
56	MG	DA	3315	1/1	0.98	0.04	31,31,31,31	0
56	MG	BA	3400	1/1	0.98	0.06	24,24,24,24	0
56	MG	BA	3544	1/1	0.98	0.13	27,27,27,27	0
56	MG	BA	3229	1/1	0.98	0.13	22,22,22,22	0
56	MG	DA	3320	1/1	0.98	0.12	30,30,30,30	0
56	MG	AA	3091	1/1	0.98	0.06	75,75,75,75	0
56	MG	BA	3403	1/1	0.98	0.11	41,41,41,41	0
56	MG	BQ	204	1/1	0.98	0.04	12,12,12,12	0
56	MG	BA	3096	1/1	0.98	0.17	62,62,62,62	0
56	MG	BA	3315	1/1	0.98	0.08	37,37,37,37	0
56	MG	DA	3625	1/1	0.98	0.09	35,35,35,35	0
56	MG	DA	3090	1/1	0.98	0.10	47,47,47,47	0
56	MG	BA	3477	1/1	0.98	0.05	25,25,25,25	0
56	MG	DA	3475	1/1	0.98	0.10	36,36,36,36	0
56	MG	BR	203	1/1	0.98	0.06	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3478	1/1	0.98	0.10	29,29,29,29	0
56	MG	BA	3406	1/1	0.98	0.05	28,28,28,28	0
56	MG	DA	3331	1/1	0.98	0.07	34,34,34,34	0
56	MG	BA	3722	1/1	0.98	0.08	32,32,32,32	0
56	MG	BA	3723	1/1	0.98	0.08	49,49,49,49	0
56	MG	BA	3359	1/1	0.98	0.05	23,23,23,23	0
56	MG	BU	205	1/1	0.98	0.09	42,42,42,42	0
56	MG	DA	3336	1/1	0.98	0.06	27,27,27,27	0
56	MG	DA	3337	1/1	0.98	0.06	27,27,27,27	0
56	MG	DA	3338	1/1	0.98	0.06	29,29,29,29	0
56	MG	BA	3725	1/1	0.98	0.09	49,49,49,49	0
56	MG	BA	3316	1/1	0.98	0.05	28,28,28,28	0
56	MG	DA	3341	1/1	0.98	0.08	23,23,23,23	0
56	MG	DA	3101	1/1	0.98	0.08	48,48,48,48	0
56	MG	BA	3556	1/1	0.98	0.14	27,27,27,27	0
56	MG	BA	3410	1/1	0.98	0.05	27,27,27,27	0
56	MG	BV	202	1/1	0.98	0.14	56,56,56,56	0
56	MG	DA	3347	1/1	0.98	0.11	62,62,62,62	0
56	MG	BA	3026	1/1	0.98	0.08	36,36,36,36	0
56	MG	BV	204	1/1	0.98	0.13	20,20,20,20	0
56	MG	BA	3485	1/1	0.98	0.13	44,44,44,44	0
56	MG	BW	202	1/1	0.98	0.15	34,34,34,34	0
56	MG	BA	3362	1/1	0.98	0.07	43,43,43,43	0
56	MG	BA	3363	1/1	0.98	0.07	39,39,39,39	0
56	MG	DA	3354	1/1	0.98	0.05	27,27,27,27	0
56	MG	DA	3355	1/1	0.98	0.10	18,18,18,18	0
56	MG	AA	3056	1/1	0.98	0.07	39,39,39,39	0
56	MG	BA	3421	1/1	0.98	0.08	36,36,36,36	0
56	MG	BA	3565	1/1	0.98	0.04	55,55,55,55	0
56	MG	BA	3491	1/1	0.98	0.08	23,23,23,23	0
56	MG	BA	3567	1/1	0.98	0.13	37,37,37,37	0
56	MG	BA	3492	1/1	0.98	0.12	23,23,23,23	0
56	MG	BA	3569	1/1	0.98	0.12	19,19,19,19	0
56	MG	BA	3570	1/1	0.98	0.07	61,61,61,61	0
56	MG	BA	3077	1/1	0.98	0.10	39,39,39,39	0
56	MG	BA	3572	1/1	0.98	0.12	36,36,36,36	0
56	MG	B3	101	1/1	0.98	0.10	28,28,28,28	0
56	MG	BA	3425	1/1	0.98	0.14	36,36,36,36	0
56	MG	DA	3234	1/1	0.98	0.10	33,33,33,33	0
56	MG	DD	305	1/1	0.98	0.21	49,49,49,49	0
56	MG	BA	3325	1/1	0.98	0.12	58,58,58,58	0
56	MG	CA	3090	1/1	0.98	0.08	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3261	1/1	0.98	0.24	34,34,34,34	0
56	MG	BB	3007	1/1	0.98	0.04	47,47,47,47	0
56	MG	BA	3428	1/1	0.98	0.08	45,45,45,45	0
56	MG	B7	102	1/1	0.98	0.06	40,40,40,40	0
56	MG	DA	3019	1/1	0.98	0.05	30,30,30,30	0
56	MG	AA	3182	1/1	0.98	0.05	49,49,49,49	0
56	MG	DE	306	1/1	0.98	0.06	32,32,32,32	0
56	MG	DA	3379	1/1	0.98	0.08	28,28,28,28	0
56	MG	BA	3431	1/1	0.98	0.11	17,17,17,17	0
56	MG	DA	3382	1/1	0.98	0.05	25,25,25,25	0
56	MG	BA	3369	1/1	0.98	0.06	45,45,45,45	0
56	MG	DA	3384	1/1	0.98	0.05	23,23,23,23	0
56	MG	DF	306	1/1	0.98	0.11	50,50,50,50	0
56	MG	DA	3245	1/1	0.98	0.08	37,37,37,37	0
56	MG	CA	3098	1/1	0.98	0.13	46,46,46,46	0
56	MG	BA	3581	1/1	0.98	0.04	51,51,51,51	0
56	MG	BA	3015	1/1	0.98	0.24	44,44,44,44	0
56	MG	DA	3026	1/1	0.98	0.06	37,37,37,37	0
56	MG	DA	3250	1/1	0.98	0.05	31,31,31,31	0
56	MG	CA	3001	1/1	0.98	0.09	55,55,55,55	0
56	MG	DA	3392	1/1	0.98	0.08	35,35,35,35	0
56	MG	DA	3540	1/1	0.98	0.21	54,54,54,54	0
56	MG	BA	3371	1/1	0.98	0.06	15,15,15,15	0
56	MG	DA	3394	1/1	0.98	0.06	47,47,47,47	0
56	MG	BA	3585	1/1	0.98	0.05	51,51,51,51	0
56	MG	BA	3436	1/1	0.98	0.04	37,37,37,37	0
56	MG	BA	3437	1/1	0.98	0.06	42,42,42,42	0
56	MG	BA	3329	1/1	0.98	0.10	29,29,29,29	0
56	MG	BA	3330	1/1	0.98	0.08	39,39,39,39	0
56	MG	AA	3010	1/1	0.98	0.10	70,70,70,70	0
56	MG	BA	3441	1/1	0.98	0.14	25,25,25,25	0
56	MG	BA	3443	1/1	0.98	0.09	26,26,26,26	0
56	MG	DA	3037	1/1	0.98	0.18	35,35,35,35	0
56	MG	DA	3262	1/1	0.98	0.08	44,44,44,44	0
56	MG	DA	3406	1/1	0.98	0.06	40,40,40,40	0
57	SF4	CD	501	8/8	0.98	0.04	64,75,91,95	0
58	ZN	AN	102	1/1	0.98	0.03	90,90,90,90	0
56	MG	AA	3156	1/1	0.98	0.11	62,62,62,62	0
56	MG	BA	3595	1/1	0.98	0.11	41,41,41,41	0
58	ZN	DY	501	1/1	0.98	0.03	83,83,83,83	0
56	MG	BA	3596	1/1	0.98	0.05	51,51,51,51	0
56	MG	DA	3411	1/1	0.98	0.05	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3213	1/1	0.98	0.07	41,41,41,41	0
56	MG	DA	3561	1/1	0.98	0.07	45,45,45,45	0
56	MG	DA	3413	1/1	0.98	0.08	53,53,53,53	0
56	MG	B8	103	1/1	0.99	0.06	24,24,24,24	0
56	MG	BA	3472	1/1	0.99	0.06	30,30,30,30	0
56	MG	BA	3323	1/1	0.99	0.06	23,23,23,23	0
56	MG	BA	3381	1/1	0.99	0.05	37,37,37,37	0
56	MG	BB	3011	1/1	0.99	0.08	37,37,37,37	0
56	MG	DA	3506	1/1	0.99	0.04	59,59,59,59	0
56	MG	AX	109	1/1	0.99	0.07	43,43,43,43	0
56	MG	BA	3310	1/1	0.99	0.10	13,13,13,13	0
56	MG	BA	3516	1/1	0.99	0.03	47,47,47,47	0
56	MG	DA	3380	1/1	0.99	0.04	26,26,26,26	0
56	MG	BA	3561	1/1	0.99	0.08	24,24,24,24	0
56	MG	BA	3342	1/1	0.99	0.06	31,31,31,31	0
56	MG	BA	3656	1/1	0.99	0.04	33,33,33,33	0
56	MG	BA	3442	1/1	0.99	0.09	12,12,12,12	0
56	MG	CA	3115	1/1	0.99	0.03	55,55,55,55	0
56	MG	BA	3343	1/1	0.99	0.08	40,40,40,40	0
56	MG	BA	3480	1/1	0.99	0.09	17,17,17,17	0
56	MG	DA	3518	1/1	0.99	0.03	40,40,40,40	0
56	MG	BA	3344	1/1	0.99	0.05	30,30,30,30	0
56	MG	BA	3411	1/1	0.99	0.08	38,38,38,38	0
56	MG	BA	3412	1/1	0.99	0.09	26,26,26,26	0
56	MG	DA	3047	1/1	0.99	0.06	34,34,34,34	0
56	MG	DA	3271	1/1	0.99	0.10	37,37,37,37	0
56	MG	BA	3447	1/1	0.99	0.06	37,37,37,37	0
56	MG	BA	3413	1/1	0.99	0.05	20,20,20,20	0
56	MG	BA	3414	1/1	0.99	0.09	19,19,19,19	0
56	MG	BA	3487	1/1	0.99	0.07	31,31,31,31	0
56	MG	DA	3397	1/1	0.99	0.11	41,41,41,41	0
56	MG	BA	3716	1/1	0.99	0.05	27,27,27,27	0
56	MG	DA	3600	1/1	0.99	0.03	45,45,45,45	0
56	MG	BA	3092	1/1	0.99	0.08	51,51,51,51	0
56	MG	BA	3302	1/1	0.99	0.06	27,27,27,27	0
56	MG	BA	3575	1/1	0.99	0.09	51,51,51,51	0
56	MG	BA	3531	1/1	0.99	0.15	38,38,38,38	0
56	MG	AA	3144	1/1	0.99	0.06	48,48,48,48	0
56	MG	BA	3418	1/1	0.99	0.08	27,27,27,27	0
56	MG	BA	3534	1/1	0.99	0.04	41,41,41,41	0
56	MG	AA	3152	1/1	0.99	0.04	19,19,19,19	0
56	MG	DA	3407	1/1	0.99	0.09	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3493	1/1	0.99	0.11	15,15,15,15	0
56	MG	DA	3345	1/1	0.99	0.03	31,31,31,31	0
56	MG	DA	3612	1/1	0.99	0.02	39,39,39,39	0
56	MG	BA	3420	1/1	0.99	0.09	33,33,33,33	0
56	MG	AV	101	1/1	0.99	0.09	36,36,36,36	0
56	MG	BA	3350	1/1	0.99	0.03	47,47,47,47	0
56	MG	DA	3289	1/1	0.99	0.03	26,26,26,26	0
56	MG	BA	3586	1/1	0.99	0.08	29,29,29,29	0
56	MG	BA	3423	1/1	0.99	0.08	26,26,26,26	0
56	MG	BA	3681	1/1	0.99	0.12	40,40,40,40	0
56	MG	DA	3548	1/1	0.99	0.03	37,37,37,37	0
56	MG	BA	3424	1/1	0.99	0.07	15,15,15,15	0
56	MG	DA	3418	1/1	0.99	0.12	29,29,29,29	0
56	MG	BA	3460	1/1	0.99	0.05	33,33,33,33	0
56	MG	BA	3081	1/1	0.99	0.03	14,14,14,14	0
56	MG	BA	3317	1/1	0.99	0.10	40,40,40,40	0
56	MG	DA	3486	1/1	0.99	0.02	38,38,38,38	0
56	MG	BA	3318	1/1	0.99	0.04	33,33,33,33	0
56	MG	DA	3556	1/1	0.99	0.03	56,56,56,56	0
56	MG	DA	3629	1/1	0.99	0.06	19,19,19,19	0
56	MG	BA	3396	1/1	0.99	0.08	22,22,22,22	0
56	MG	BA	3319	1/1	0.99	0.07	25,25,25,25	0
56	MG	DA	3300	1/1	0.99	0.06	37,37,37,37	0
56	MG	AA	3192	1/1	0.99	0.07	57,57,57,57	0
56	MG	BA	3321	1/1	0.99	0.09	29,29,29,29	0
57	SF4	AD	501	8/8	0.99	0.04	59,72,92,96	0
56	MG	BA	3337	1/1	0.99	0.07	23,23,23,23	0
56	MG	BA	3434	1/1	0.99	0.04	32,32,32,32	0
58	ZN	BY	202	1/1	0.99	0.02	71,71,71,71	0
56	MG	BA	3378	1/1	0.99	0.02	20,20,20,20	0
58	ZN	B5	501	1/1	0.99	0.02	54,54,54,54	0
56	MG	BA	3553	1/1	0.99	0.03	31,31,31,31	0
56	MG	DA	3639	1/1	0.99	0.13	15,15,15,15	0
56	MG	DA	3368	1/1	0.99	0.04	39,39,39,39	0
58	ZN	D5	103	1/1	0.99	0.02	70,70,70,70	0
58	ZN	D6	501	1/1	0.99	0.04	61,61,61,61	0
58	ZN	D9	501	1/1	0.99	0.04	66,66,66,66	0
56	MG	BA	3695	1/1	0.99	0.10	15,15,15,15	0
56	MG	DA	3568	1/1	0.99	0.04	42,42,42,42	0
56	MG	AA	3165	1/1	0.99	0.08	23,23,23,23	0
56	MG	DA	3083	1/1	0.99	0.04	41,41,41,41	0
56	MG	BA	3429	1/1	1.00	0.05	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3356	1/1	1.00	0.02	27,27,27,27	0
56	MG	BA	3583	1/1	1.00	0.07	27,27,27,27	0
56	MG	DA	3190	1/1	1.00	0.02	37,37,37,37	0
56	MG	BA	3520	1/1	1.00	0.07	34,34,34,34	0
56	MG	DA	3317	1/1	1.00	0.03	32,32,32,32	0
56	MG	DA	3263	1/1	1.00	0.05	31,31,31,31	0
56	MG	BA	3407	1/1	1.00	0.06	15,15,15,15	0
58	ZN	B6	501	1/1	1.00	0.04	49,49,49,49	0
58	ZN	B9	501	1/1	1.00	0.03	48,48,48,48	0

6.5 Other polymers (i)

There are no such residues in this entry.